

QITE

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Celine Qian Examiner #: 78760 Date: 12/17/04
Art Unit: 1636 Phone Number: 202-0777 Serial Number: 10/030658
Mail Box and Bldg/Room Location: 2A 64 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Trap vector & gene trapping using the same
Inventors (please provide full names): Yamamura et al.

Earliest Priority Filing Date: 7/14/99

For Seq. only Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

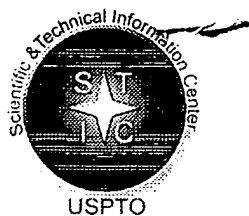
Please search SEQ ID NO: 1 & 2.

1 - NA - 13
2 - NA - 13
ME

STAFF USE ONLY

Staff Use Only	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) <u>2</u> STN _____	
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>12/22/04</u>	Bibliographic _____	Dr.Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep. Review Time: _____	Fulltext _____	Sequence Systems <u>01</u> _____
Central Prep. Time: _____	Patent Family _____	WWW/Internet _____
Other Time: _____	Other _____	Other (specify) _____

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STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 140626

TO: Celine Qian
Location: REM/2A64/2C70
Art Unit: 1636
Monday, December 27, 2004

Case Serial Number: 10/030658

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov



Search Notes

Examiner Qian,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



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GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 05:35:57 ; Search time 864.5 Seconds
(without alignments)
711.123 Million cell updates/sec

Title: US-10-030-658B-1

Perfect score: 13
Sequence: 1 taccggtcgata 13

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba.*
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3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
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9: gb_pr.*
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13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	13	100.0	13	6	BD091728
3	13	100.0	33	6	AX662245
4	13	100.0	33	6	AX662246
5	13	100.0	34	6	BD182868
6	13	100.0	34	6	BD182869
7	13	100.0	34	6	BD182873
8	13	100.0	34	6	BD182873
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c	22	13	100.0	34	6	AX540641	Sequence
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c	24	13	100.0	34	6	AX710009	Sequence
c	25	13	100.0	34	6	AX710011	Sequence
c	26	13	100.0	34	6	BD083072	Antisense
c	27	13	100.0	34	6	BD083073	Antisense
c	28	13	100.0	34	6	BD091732	Trap vect.
c	29	13	100.0	34	6	BD091732	Trap vect.
c	30	13	100.0	34	6	BD093611	Antisense
c	31	13	100.0	34	6	BD093612	Antisense
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c	33	13	100.0	44	6	AX710017	Sequence
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c	35	13	100.0	67	6	AX710015	Sequence
c	36	13	100.0	68	6	AX710014	Sequence
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ALIGNMENTS

RESULT 1
BD091727 13 bp DNA linear PAT 27-AUG-2002
LOCUS Trap vector and gene trapping method by using the same.
DEFINITION BD091727
ACCESSION BD091727 GI:22637338
VERSION WO 0105987-A/1.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 13)
AUTHORS Yamamura, K. and Araki, K.
TITLE Trap vector and gene trapping method by using the same
JOURNAL Patent: WO 0105987-A 1 25-JAN-2001;
KUMAMOTO TECHNOLOGICAL FOUNDATION, KENICHI YAMAMURA, KIMI ARAKI
COMMENT OS Artificial Sequence
PN WO 0105987-A/1
PD 25-JAN-2001
PF 02-MAY-2000 WO 2000JP002916
PR 14-JUL-1999 JP 99P 200997
PI KENICHI YAMAMURA, KIMI ARAKI
PC Cl2N15/85,A01K67/027
CC Description of Artificial Sequence:synthetic DNA FH Key
Location/Qualifiers

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Trap vector and gene trapping method by using the same.

DEFINITION BD091728.1 GI:22637339
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE 1 (bases 1 to 13)
AUTHORS Yamamura,K. and Araki,K.
TITLE Trap vector and gene trapping method by using the same
JOURNAL Patent: WO 0105987-A 2 25-JAN-2001;
KUMAMOTO TECHNOLOGICAL FOUNDATION,KENICHI YAMAMURA,KIMI ARAKI

COMMENT OS Artificial Sequence
PN WO 0105987-A/2
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PI KENICHI YAMAMURA,KIMI ARAKI
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LOCUS
DEFINITION Sequence 1 from Patent WO02083889.

ACCESSION AX662245
VERSION AX662245.1 GI:29163144
KEYWORDS
SOURCE
ORGANISM

REFERENCE 1
AUTHORS Bigger,B.W., Tolmachov,O. and Coutelle,C.
TITLE Methods
JOURNAL Patent: WO 02083889-A 1 24-OCT-2002;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)

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LOCUS

DEFINITION Sequence 2 from Patent WO02083889.

ACCESSION AX662246
VERSION AX662246.1 GI:29163145
KEYWORDS
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ORGANISM

REFERENCE 1
AUTHORS Bigger,B.W., Tolmachov,O. and Coutelle,C.
TITLE Methods
JOURNAL Patent: WO 02083889-A 2 24-OCT-2002;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)

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LOCUS
DEFINITION Knockout animal.
ACCESSION BD182868
VERSION BD182868.1 GI:31875068
KEYWORDS JP 2002345477-A/1.
SOURCE
ORGANISM

REFERENCE 1
AUTHORS Ide,H., Yamamura,K. and Araki,K.
TITLE Knockout animal
JOURNAL Patent: JP 2002345477-A 1 03-DEC-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP,HIROYUKI IDE,KENICHI YAMAMURA,
KIMI ARAKI

COMMENT OS Artificial Sequence
PN JP 2002345477-A/1
PD 03-DEC-2002
PF 25-MAY-2001 JP 2001157567
PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
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DEFINITION  Knockout animal.
ACCESSION   BD182869
VERSION     BD182869.1 GI:31875069
KEYWORDS    JP 2002345477-A/2.
SOURCE      synthetic construct
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REFERENCE   1 (bases 1 to 34)
            Ide,H., Yamamura,K. and Araki,K.
AUTHORS     Knockout animal
TITLE       Patent: JP 2002345477-A 2 03-DEC-2002;
JOURNAL     JAPAN SCIENCE AND TECHNOLOGY CORP,HIROYUKI IDE,KENICHI YAMAMURA,
            KIMI ARAKI
COMMENT     OS Artificial Sequence
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DEFINITION  Knockout animal.
ACCESSION   BD182873
VERSION     BD182873.1 GI:31875073
KEYWORDS    JP 2002345477-A/6.
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 34)
            Ide,H., Yamamura,K. and Araki,K.
AUTHORS     Knockout animal
TITLE       Patent: JP 2002345477-A 6 03-DEC-2002;
JOURNAL     JAPAN SCIENCE AND TECHNOLOGY CORP,HIROYUKI IDE,KENICHI YAMAMURA,
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COMMENT     OS Artificial Sequence
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 34 TACCGTTCGTATA 22

RESULT 8
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DEFINITION  Knockout animal.
ACCESSION   BD182873
VERSION     BD182873.1 GI:31875073
KEYWORDS    JP 2002345477-A/6.
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 34)
            Ide,H., Yamamura,K. and Araki,K.
AUTHORS     Knockout animal
TITLE       Patent: JP 2002345477-A 6 03-DEC-2002;
JOURNAL     JAPAN SCIENCE AND TECHNOLOGY CORP,HIROYUKI IDE,KENICHI YAMAMURA,
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COMMENT     OS Artificial Sequence
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DB 34 TACCGTTCGTATA 22

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DEFINITION  Knockout animal.
ACCESSION   BD185622
VERSION     BD185622.1 GI:31877822
KEYWORDS    JP 2002369689-A/1.
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 34)
            Ide,H., Yamamura,K. and Araki,K.
AUTHORS     Knockout animal
TITLE       Patent: JP 2002369689-A 1 24-DEC-2002;
JOURNAL     JAPAN SCIENCE AND TECHNOLOGY CORP,EU GENE LTD, PRESIDENT OF
            KUMAMOTO UNIVERSITY
COMMENT     OS Artificial Sequence
            PN JP 2002369689-A/1
            PD 24-DEC-2002
            PF 25-MAY-2001 JP 2001157568
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DEFINITION  Knockout animal.
ACCESSION   BD182869
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SOURCE      synthetic construct
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REFERENCE   1 (bases 1 to 34)
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AUTHORS     Knockout animal
TITLE       Patent: JP 2002345477-A 2 03-DEC-2002;
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QY 1 TACCGTTCGTATA 13
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DB 34 TACCGTTCGTATA 22

RESULT 7
BD182873
LOCUS       BD182873                      34 bp    DNA          linear          PAT 17-JUN-2003
DEFINITION  Knockout animal.
ACCESSION   BD182873
VERSION     BD182873.1 GI:31875073
KEYWORDS    JP 2002345477-A/6.
SOURCE      synthetic construct
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AUTHORS     Knockout animal
TITLE       Patent: JP 2002345477-A 6 03-DEC-2002;
JOURNAL     JAPAN SCIENCE AND TECHNOLOGY CORP,HIROYUKI IDE,KENICHI YAMAMURA,
            KIMI ARAKI
COMMENT     OS Artificial Sequence
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RESULT 8
BD182873/c
LOCUS       BD182873/c                    34 bp    DNA          linear          PAT 17-JUN-2003
DEFINITION  Knockout animal.
ACCESSION   BD182873
VERSION     BD182873.1 GI:31875073
KEYWORDS    JP 2002345477-A/6.
SOURCE      synthetic construct
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TITLE       Patent: JP 2002345477-A 6 03-DEC-2002;
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DB 34 TACCGTTCGTATA 22

RESULT 9
BD185622
LOCUS       BD185622                      34 bp    DNA          linear          PAT 17-JUN-2003
DEFINITION  Knockout animal.
ACCESSION   BD185622
VERSION     BD185622.1 GI:31877822
KEYWORDS    JP 2002369689-A/1.
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 34)
            Ide,H., Yamamura,K. and Araki,K.
AUTHORS     Knockout animal
TITLE       Patent: JP 2002369689-A 1 24-DEC-2002;
JOURNAL     JAPAN SCIENCE AND TECHNOLOGY CORP,EU GENE LTD, PRESIDENT OF
            KUMAMOTO UNIVERSITY
COMMENT     OS Artificial Sequence
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            PD 24-DEC-2002
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AUTHORS		Ide,H., Yamamura,K. and Araki,K.	
TITLE		Knockout animal	
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DB		1 TACCGTTCGTATA 13	
RESULT 12			
BD185627/c		34 bp DNA linear PAT 17-JUN-2003	
LOCUS		Knockout animal.	
DEFINITION		BD185627	
ACCESSION		BD185627.1 GI:31877827	
VERSION		JP 2002369689-A/6.	
KEYWORDS		synthetic construct	
SOURCE		synthetic construct	
ORGANISM		artificial sequences.	
REFERENCE		1 (bases 1 to 34)	
AUTHORS		Ide,H., Yamamura,K. and Araki,K.	
TITLE		Knockout animal	
JOURNAL		Patent: JP 2002369689-A 6 24-DEC-2002;	
		JAPAN SCIENCE AND TECHNOLOGY CORP,EU GENE LTD, PRESIDENT OF	
COMMENT		KUMAMOTO UNIVERSITY	
		OS Artificial Sequence	
		PN JP 2002369689-A/6	
		PD 24-DEC-2002	
		PF 25-MAY-2001 JP 2001157568	
		PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI	
		PC C12N15/09,A01K67/027,C12N5/10,C12N15/00,C12N5/00 CC	
		Description of Artificial Sequence:synthetic DNA FH Key	
Location/Qualifiers		1. .34	
FT source		/organism='Artificial Sequence'.	
FT		Location/Qualifiers	
FEATURES		1. .34	
source		/organism="synthetic construct"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:32630"	
ORIGIN			
Query Match		100.0%; Score 13; DB 6; Length 34;	
Best Local Similarity		100.0%; Pred. No. 3.2e+03;	
Matches 13; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY		1 TACCGTTCGTATA 13	
DB		34 TACCGTTCGTATA 22	


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RESULT 13
AX114842/c
LOCUS       AX114842               34 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION   Sequence 2 from Patent WO0129208.
ACCESSION   AX114842
VERSION     AX114842.1  GI:14031784
KEYWORDS
ORGANISM     synthetic construct
SOURCE       synthetic construct
            artificial sequences.
REFERENCE    1
AUTHORS      Kuehn,R., von Melchener,H. and Altschmied,J.
TITLE        Conditional gene trapping construct for the disruption of genes
JOURNAL      Patent: WO 0129208-A 2 26-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES
SOURCE      1..34
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="mutant loxp site - lox66"
ORIGIN
Query Match      100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TACCGTTCGTATA 13
        |||||
DB      34 TACCGTTCGTATA 22
        |||||
RESULT 14
AX114843
LOCUS       AX114843               34 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION   Sequence 3 from Patent WO0129208.
ACCESSION   AX114843
VERSION     AX114843.1  GI:14031785
KEYWORDS
SOURCE       synthetic construct
            artificial sequences.
ORGANISM     synthetic construct
REFERENCE    1
AUTHORS      Kuehn,R., von Melchener,H. and Altschmied,J.
TITLE        Conditional gene trapping construct for the disruption of genes
JOURNAL      Patent: WO 0129208-A 3 26-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES
SOURCE      1..34
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="mutant loxp site - lox71"
ORIGIN
Query Match      100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TACCGTTCGTATA 13
        |||||
DB      1 TACCGTTCGTATA 13
        |||||
RESULT 15
AX114844
LOCUS       AX114844               34 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION   Sequence 4 from Patent WO0129208.
ACCESSION   AX114844
VERSION     AX114844.1  GI:14031786
KEYWORDS
SOURCE       synthetic construct
            artificial sequences.
ORGANISM     synthetic construct
REFERENCE    1
AUTHORS      Kuehn,R., von Melchener,H. and Altschmied,J.
TITLE        Conditional gene trapping construct for the disruption of genes
JOURNAL      Patent: WO 0129208-A 4 26-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES
SOURCE      1..34
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="double mutant loxp site - lox66/71"
ORIGIN
Query Match      100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TACCGTTCGTATA 13
        |||||
DB      1 TACCGTTCGTATA 13
        |||||
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 05:32:27 ; Search time 212 Seconds
(without alignments)
321.898 Million cell updates/sec

Title: US-10-030-658B-1

Perfect score: 13

Sequence: 1 taccgttcgtata 13

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 23Sep04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	13	4	Aaf58480 Oligonuc
2	13	100.0	13	4	Aaf58481 Oligonuc
3	13	100.0	13	8	Abz79445 DNA seque
4	13	100.0	13	8	Abz79456 DNA seque
5	13	100.0	33	8	Abv75983 Modified
6	13	100.0	33	8	Abv75984 Modified
7	13	100.0	34	4	Aaf58485 Oligonuc
8	13	100.0	34	4	Aaf58485 Oligonuc
9	13	100.0	34	5	Aad04917 Recombina
10	13	100.0	34	5	Aad04918 Recombina
11	13	100.0	34	5	Aad04918 Recombina
12	13	100.0	34	5	Aad04918 Recombina
13	13	100.0	34	6	Abn84175 Loxp left
14	13	100.0	34	6	Abn84176 Loxp right
15	13	100.0	34	6	Abn84176 Loxp right
16	13	100.0	34	6	ABA03776 Synthetic
17	13	100.0	34	6	ABA03775 Synthetic
18	13	100.0	34	8	Abv75996 Modified
19	13	100.0	34	8	Abz20929 Loxp muta
20	13	100.0	34	8	Abz20931 Loxp muta
21	13	100.0	34	8	Abz20924 Loxp muta
					Abz79444 Lox 71 DN

C	22	13	100.0	34	8	ABZ79445	Abz79445 Lox 66 DN
C	23	13	100.0	34	8	ABZ79449	Abz79449 Lox 71/66
C	24	13	100.0	34	8	ABZ79449	Abz79449 Lox 71/66
C	25	13	100.0	34	9	ACC85309	Acc85309 Recombina
C	26	13	100.0	34	9	ACC85308	Acc85308 Recombina
C	27	13	100.0	34	10	ADD13802	ADD13802 Oligonuc
C	28	13	100.0	34	10	ADD13801	ADD13801 Oligonuc
C	29	13	100.0	34	10	ADD15151	ADD15151 Variant 1
C	30	13	100.0	34	10	ADD15152	ADD15152 Variant 1
C	31	13	100.0	34	10	ADD15152	ADD15152 Variant 1
C	32	13	100.0	34	10	ADD15150	ADD15150 Variant 1
C	33	13	100.0	34	10	ABZ75320	Abz75320 Lox66 rel
C	34	13	100.0	34	10	ABZ75324	Abz75324 Lox71/66
C	35	13	100.0	34	10	ABZ75324	Abz75324 Lox71/66
C	36	13	100.0	34	10	ABZ75319	Abz75319 Lox71 rel
C	37	13	100.0	40	4	AH44859	Ah44859 PCR prime
C	38	13	100.0	44	8	ABZ20935	Abz20935 Lox66 iso
C	39	13	100.0	44	8	ABZ20936	Abz20936 Lox71 iso
C	40	13	100.0	67	8	ABZ20923	Abz20923 Lox66 and
C	41	13	100.0	68	8	ABZ20922	Abz20922 Lox66 and
C	42	13	100.0	78	5	AAD04925	Aad04925 Primer lo
C	43	13	100.0	79	5	AAD04926	Aad04926 Primer lo
C	44	13	100.0	94	8	ABV75994	Abv75994 OLIGO-F
C	45	13	100.0	94	8	ABV75994	Abv75994 OLIGO-F

ALIGNMENTS

RESULT 1

AAF58480
ID AAF58480 standard; DNA; 13 BP.
AC AAF58480;
XX
XX 24-APR-2001 (first entry)
XX Oligonucleotide: SEQ ID 1.
XX Trap vector; loxp; gene therapy; gene trapping; ds.
XX Unidentified.
XX WO200105987-A1.
XX 25-JAN-2001.
XX 02-MAY-2000; 2000WO-JP002916.
XX 14-JUL-1999; 99JP-00200997.
XX (TRAN-) TRANSGENIC INC.
XX Yamamura K, Araki K;
XX WPI; 2001-159541/16.
XX New trap vector, useful for gene trapping method for the efficient
XX production of gene-disrupted animals for investigating human diseases and
XX drug development, comprises a mutated loxp.
XX Claim 3; Page 11; 55pp; Japanese.
XX The present invention relates to a trap vector comprising a mutated loxp
XX in which a mutation is transferred into a part of a reversed repetitive
XX sequence in the loxp sequence. The vector is useful in the gene trapping
XX method for production of gene-disrupted animals in studying gene
XX functions, constructing model animals for investigating human diseases
XX and drug development, and gene therapy. The present sequence is an
XX oligonucleotide used in the present invention
XX Sequence 13 BP; 3 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

Mon Dec 27 14:12:26 2004

us-10-030-658b-1.rng

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Query Match      100.0%; Score 13; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCGTTCGTATA 13
DB      1 TACCGTTCGTATA 13

RESULT 2
AAF58481/c
ID AAF58481 standard; DNA; 13 BP.
XX
AC AAF58481;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide: SEQ ID 2.
XX
KW Trap vector; loxP; gene therapy; gene trapping; ds.
XX
OS Unidentified.
XX
PN WO200105987-A1.
XX
PD 25-JAN-2001.
XX
PF 02-MAY-2000; 2000WO-JP002916.
XX
PR 14-JUL-1999; 99JP-00200997.
XX
PA (TRAN-) TRANSGENIC INC.
XX
PI Yamamura K, Araki K;
XX
DR WPI; 2001-159541/16.
XX
PT New trap vector, useful for gene trapping method for the efficient
PT production of gene-disrupted animals for investigating human diseases and
PT drug development, comprises a mutated loxP.
XX
PS Claim 6; Page 12; 55pp; Japanese.
XX
CC The present invention relates to a trap vector comprising a mutated loxP
CC in which a mutation is transferred into a part of a reversed repetitive
CC sequence in the loxP sequence. The vector is useful in the gene trapping
CC method for production of gene-disrupted animals in studying gene
CC functions, constructing model animals for investigating human diseases
CC and drug development, and gene therapy. The present sequence is an
CC oligonucleotide used in the present invention
XX
SQ Sequence 13 BP; 5 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match      100.0%; Score 13; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCGTTCGTATA 13
DB      13 TACCGTTCGTATA 1

RESULT 3
ABZ79455
ID ABZ79455 standard; DNA; 13 BP.
XX
AC ABZ79455;
XX
DT 23-MAY-2003 (first entry)
XX
DE DNA sequence related to the chimera mouse of the invention #1.
DE LoxP; knockout mouse; vascularisation; embryonic stem cell;
XX
KW LoxP; knockout mouse; vascularisation; embryonic stem cell;

Query Match      100.0%; Score 13; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCGTTCGTATA 13
DB      13 TACCGTTCGTATA 1

RESULT 4
ABZ79456/c
ID ABZ79456 standard; DNA; 13 BP.
XX
AC ABZ79456;
XX
DT 23-MAY-2003 (first entry)
XX
DE DNA sequence related to the chimera mouse of the invention #2.
DE LoxP; knockout mouse; vascularisation; embryonic stem cell;
KW LoxP; knockout mouse; vascularisation; embryonic stem cell;
KW drug development; locus of crossing over; ds.
XX
OS Unidentified.
XX
PN JP2002369689-A.
XX
PD 24-DEC-2002.
XX
PF 25-MAY-2001; 2001JP-00157568.
XX
PR 25-MAY-2001; 2001JP-00157568.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (IDEH/) IDE H.
PA (YAMA/) YAMAMURA K.
PA (ARAK/) ARAKI Y.
XX
DR WPI; 2003-125824/12.

KW drug development; locus of crossing over; ds.
XX
OS Unidentified.
XX
PN JP2002369689-A.
XX
PD 24-DEC-2002.
XX
PF 25-MAY-2001; 2001JP-00157568.
XX
PR 25-MAY-2001; 2001JP-00157568.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (IDEH/) IDE H.
PA (YAMA/) YAMAMURA K.
PA (ARAK/) ARAKI Y.
XX
DR WPI; 2003-125824/12.

KW Knockout mouse or embryonic stem cells with introduced trap vectors
KW containing a loxP sequence or a variant loxP sequence with disrupted gene
PT of sequence No. 7 of 1405 bases.
XX
PS Disclosure; Page 6; 21pp; Japanese.
XX
CC The invention relates to a knockout mouse or embryonic stem cells with
CC introduced trap vectors containing a loxP sequence. The knockout animals
CC of the invention may be used in the analysis of genomic functions,
CC particularly for investigating the processes of vascularisation and the
CC development of drugs participating in such processes. The current
CC sequence represents a DNA sequence related to the chimera mouse of the
CC invention
XX
SQ Sequence 13 BP; 3 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

Query Match      100.0%; Score 13; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCGTTCGTATA 13
DB      1 TACCGTTCGTATA 13
```

XX Knockout mouse or embryonic stem cells with introduced trap vectors
PT containing a loxp sequence or a variant loxp sequence with disrupted gene
PT of sequence No. 7 of 1405 bases.
XX
XX
PS Disclosure; Page 6; 21pp; Japanese.
XX
XX The invention relates to a knockout mouse or embryonic stem cells with
CC introduced trap vectors containing a loxp sequence. The knockout animals
CC of the invention may be used in the analysis of genomic functions, and
CC particularly for investigating the processes of vascular function, and the
CC development of drugs participating in such processes. The current
CC sequence represents a DNA sequence related to the chimera mouse of the
CC invention
XX
XX Sequence 13 BP; 5 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 13; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TACCGTTCGTATA 13
DB 13 TACCGTTCGTATA 1
RESULT 5
ABV75983
ID ABV75983 standard; DNA; 33 BP.
XX
AC ABV75983;
XX
DT 11-FEB-2003 (first entry)
XX
DE Modified left element loxp site.
XX
XX LoxP; phage P1; recombination; minicircle; gene therapy; mitochondria;
KW mutant; ss.
XX
XX Bacteriophage p1.
OS Synthetic.
XX
XX WO200283889-A2.
PN
PD 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-GB001668.
PF
XX
XX 10-APR-2001; 2001GB-00008968.
PR
XX 05-OCT-2001; 2001US-0327029P.
XX
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
PA
XX
PI Bigger BW, Tolmachov O, Coutelle C;
XX
XX WPI; 2003-075546/07.
XX
XX New cell capable of expressing an endonuclease, useful for producing a
PT minicircle for mitochondrial gene therapy, comprises a parent plasmid
PT capable of recombination to form a minicircle and a miniplasmid.
XX
XX Disclosure; Page 4; 70pp; English.
XX
XX The present sequence is that of a left element (LE) loxp site in which
CC the 5 nucleotides at the 5' end of loxp have been modified. The LE loxp
CC site is used in the method of the invention for the production of a
CC minicircle. In this method, a parent plasmid is provided which has a
CC nucleic acid sequence flanked by recombination sites. The plasmid is
CC exposed to an enzyme which causes recombination at the recombination
CC sites, forming (i) a minicircle comprising the nucleic acid sequence and
CC (ii) a miniplasmid comprising the remainder of the parent plasmid. One
CC recombination site is modified at the 5' end such that its reaction with
CC the enzyme is less efficient than the wild-type site, and the other
CC recombination site is modified at the 5' end such that its reaction with
CC the enzyme is less efficient than the wild-type site, and the other

CC recombination site is modified at the 3' end such that its reaction with
CC the enzyme is less efficient than the wild-type site, both modified sites
CC being located in the minicircle after recombination. This favours the
CC formation of the minicircle. In a preferred embodiment, the enzyme is Cre
CC recombinase and the recombination sites are loxp sites. The method is
CC preferably carried out in a bacterium, especially Escherichia coli. The
CC minicircle can be used for mitochondrial gene therapy
XX
SQ Sequence 33 BP; 10 A; 6 C; 5 G; 12 T; 0 U; 0 Other;
Query Match 100.0%; Score 13; DB 8; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TACCGTTCGTATA 13
DB 1 TACCGTTCGTATA 13
RESULT 6
ABV75984/c
ID ABV75984 standard; DNA; 33 BP.
XX
AC ABV75984;
XX
DT 11-FEB-2003 (first entry)
XX
DE Modified right element loxp site.
XX
XX LoxP; phage P1; recombination; minicircle; gene therapy; mitochondria;
KW mutant; ss.
XX
XX Bacteriophage p1.
OS Synthetic.
XX
XX WO200283889-A2.
PN
PD 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-GB001668.
PF
XX
XX 10-APR-2001; 2001GB-00008968.
PR
XX 05-OCT-2001; 2001US-0327029P.
XX
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
PA
XX
PI Bigger BW, Tolmachov O, Coutelle C;
XX
XX WPI; 2003-075546/07.
XX
XX New cell capable of expressing an endonuclease, useful for producing a
PT minicircle for mitochondrial gene therapy, comprises a parent plasmid
PT capable of recombination to form a minicircle and a miniplasmid.
XX
XX Disclosure; Page 4; 70pp; English.
XX
XX The present sequence is that of a right element (RE) loxp site in which
CC the 5 nucleotides at the 3' end of loxp have been modified. The RE loxp
CC site is used in the method of the invention for the production of a
CC minicircle. In this method, a parent plasmid is provided which has a
CC nucleic acid sequence flanked by recombination sites. The plasmid is
CC exposed to an enzyme which causes recombination at the recombination
CC sites, forming (i) a minicircle comprising the nucleic acid sequence and
CC (ii) a miniplasmid comprising the remainder of the parent plasmid. One
CC recombination site is modified at the 5' end such that its reaction with
CC the enzyme is less efficient than the wild-type site, and the other
CC recombination site is modified at the 3' end such that its reaction with
CC the enzyme is less efficient than the wild-type site, both modified sites
CC being located in the minicircle after recombination. This favours the
CC formation of the minicircle. In a preferred embodiment, the enzyme is Cre
CC recombinase and the recombination sites are loxp sites. The method is
CC preferably carried out in a bacterium, especially Escherichia coli. The
CC minicircle can be used for mitochondrial gene therapy

CC recombinase which is capable of unidirectional inversion of double
 CC standard DNA segment. One of the DNA segment (disruption cassette) is
 CC inserted in antisense orientation relative to the transcriptional
 CC orientation of the gene to be trapped. The other DNA segment (selection
 CC cassette) is inserted in sense direction relative to the transcriptional
 CC orientation of the gene to be trapped. The cell comprising the gene
 CC trapping construct is useful for the identification and/or isolation of
 CC genes. The transgenic organism comprising the gene trapping construct is
 CC useful to study gene function at various developmental stages. The gene
 CC trapping construct is useful for mutationally inactivating all cellular
 CC genes. The present DNA sequence encodes recombinase recognition sequence,
 CC loxP site mutant (lox66), which flanks the functional DNA segments of
 CC gene trapping construct
 XX Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 13; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TACCGTTCGTATA 13
 DB 34 TACCGTTCGTATA 22
 RESULT 13
 ABN84175/C
 ID ABN84175 standard; DNA; 34 BP.
 XX AC ABN84175;
 XX DT 23-SEP-2002 (first entry)
 XX DE LoxP left element mutant.
 XX KW Gene inactivation; mutagenesis; vector; knockout animal;
 XX KW transgenic animal; gene trapping; loxP; mutant; ss.
 XX OS Enterobacteria phage P1.
 XX OS Synthetic.
 XX PN WO200240685-A2.
 XX PD 23-MAY-2002.
 XX PF 16-NOV-2001; 2001WO-US043916.
 XX PF 16-NOV-2000; 2000US-0249200P.
 XX PR (CORR) CORNELL RES FOUND INC.
 XX PA Xin H, Kotlikoff M;
 XX PI WPI; 2002-537342/57.
 XX DR Novel genetically engineered vector comprising gene trap cassette, and
 XX PT mutational element cassette that is transcriptionally silent, but which
 XX PT is activated by recombinase expression to disrupt expression of trapped
 XX PT gene.
 XX PS Example 2; Page 35; 58pp; English.
 XX SS The present invention provides recombinant vectors and methods of using
 CC the vectors in a high-throughput genetic system to rapidly generate
 CC conditional and/or conventional knockout mutants, e.g. in mice, useful
 CC for identifying and defining mammalian gene function in vivo. The methods
 CC combine gene trapping, gene targeting, and site-specific recombination
 CC techniques. The vectors comprise a transcriptionally silent mutational
 CC element that is inserted within a gene in a target cell in a manner that
 CC retains gene function, and which can be manipulated to inactivate the
 CC gene when desired. The mutational element may be flanked by mutant LoxP
 CC sites in a manner that produces a directional bias toward inversion of
 CC the mutational sequence upon exposure to cre recombinase. Once inverted,

XX The present invention relates to a conditional gene trapping construct
 CC capable of causing conditional mutations in genes. The gene trapping
 CC construct comprises two functional DNA segments, each being flanked by
 CC two recombinase recognition sequences (RRSs) specific to site specific
 CC recombinase which is capable of unidirectional inversion of double
 CC standard DNA segment. One of the DNA segment (disruption cassette) is
 CC inserted in antisense orientation relative to the transcriptional
 CC orientation of the gene to be trapped. The other DNA segment (selection
 CC cassette) is inserted in sense direction relative to the transcriptional
 CC orientation of the gene to be trapped. The cell comprising the gene
 CC trapping construct is useful for the identification and/or isolation of
 CC genes. The transgenic organism comprising the gene trapping construct is
 CC useful to study gene function at various developmental stages. The gene
 CC trapping construct is useful for mutationally inactivating all cellular
 CC genes. The present DNA sequence encodes recombinase recognition sequence,
 CC loxP site double mutant (lox71/lox66), which flanks the functional DNA
 CC segments of gene trapping construct
 XX Sequence 34 BP; 11 A; 7 C; 6 G; 10 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 13; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TACCGTTCGTATA 13
 DB 34 TACCGTTCGTATA 22
 RESULT 12
 AAD04916/C
 ID AAD04916 standard; DNA; 34 BP.
 XX AC AAD04916;
 XX DT 17-JUL-2001 (first entry)
 XX DE Recombinase recognition sequence (RRS), loxP site mutant (lox66) DNA.
 XX KW Gene trapping construct; conditional mutation; unidirectional inversion;
 XX KW recombinase recognition sequence; RRS; disruption cassette;
 XX KW selection cassette; transgenic organism; loxP site; mutant; ds.
 XX OS Enterobacteria phage P1.
 XX OS Synthetic.
 XX PN WO200129208-A1.
 XX PD 26-APR-2001.
 XX PF 16-OCT-2000; 2000WO-EP010162.
 XX PR 16-OCT-1999; 99EP-00120592.
 XX PR 27-OCT-1999; 99US-0162016P.
 XX PA (ARTE-) ARTEMIS PHARM GMBH
 XX PA (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
 XX PI Kuehn R, Von Melchner H, Altschmidt J;
 XX PI WPI; 2001-308486/32.
 XX DR New gene trapping construct capable of causing conditional mutations in
 XX PT genes, comprises functional DNA segment inserted in sense or antisense
 XX PT direction relative to gene to be trapped.
 XX PS Claim 4; Page 49; 78pp; English.
 XX SS The present invention relates to a conditional gene trapping construct
 CC capable of causing conditional mutations in genes. The gene trapping
 CC construct comprises two functional DNA segments, each being flanked by
 CC two recombinase recognition sequences (RRSs) specific to site specific

CC the mutational element is spliced into the trapped gene resulting in
 CC expression of a reporter gene and premature termination of the endogenous
 CC mRNA. Site-directed DNA integration is achieved using a pair of mutant
 CC loxP sites, a right element (RE) mutant (see ABN84176) and a left element
 CC (LE) mutant (present sequence). The mutant loxP system produces a
 CC reaction biased toward an irreversible gene inversion. The method of the
 CC invention facilitates investigation of the function of individual genes
 CC by a rapid extension of the conditional knockout approach

XX Sequence 34 BP; 12 A; 5 C; 6 G; 11 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 13; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
 DB 34 TACCGTTCGTATA 22

RESULT 14

ABN84176/c
 ID ABN84176 standard; DNA; 34 BP.

XX AC

XX 23-SBP-2002 (first entry)

XX DE LoxP right element mutant.

XX Gene inactivation; mutagenesis; vector; knockout animal;
 KW transgenic animal; gene trapping; loxP; mutant; ss.

XX Enterobacteria phage P1.

XX Synthetic.

XX WO200240685-A2.

XX 23-MAY-2002.

XX 16-NOV-2001; 2001WO-US043916.

XX 16-NOV-2000; 2000US-0249200P.

XX (CORR) CORNELL RES FOUND INC.

XX Xin H, Kotlikoff M;

XX WPI; 2002-537342/57.

XX Novel genetically engineered vector comprising gene trap cassette, and
 PT mutational element cassette that is transcriptionally silent, but which
 PT is activated by recombinase expression to disrupt expression of trapped
 PT gene.

PS Example 2; Page 35; 58pp; English.

XX The present invention provides recombinant vectors and methods of using
 CC the vectors in a high-throughput genetic system to rapidly generate
 CC conditional and/or conventional knockout mutants, e.g. in mice, useful
 CC for identifying and defining mammalian gene function in vivo. The methods
 CC combine gene trapping, gene targeting, and site-specific recombination
 CC techniques. The vectors comprise a transcriptionally silent mutational
 CC element that is inserted within a gene in a target cell in a manner that
 CC retains gene function, and which can be manipulated to inactivate the
 CC gene when desired. The mutational element may be flanked by mutant loxP
 CC sites in a manner that produces a directional bias toward inversion of
 CC the mutational sequence upon exposure to cre recombinase. Once inverted,
 CC the mutational element is spliced into the trapped gene resulting in
 CC expression of a reporter gene and premature termination of the endogenous
 CC mRNA. Site-directed DNA integration is achieved using a pair of mutant
 CC loxP sites, a right element (RE) mutant (present sequence) and a left
 CC element (LE) mutant (see ABN84175). The mutant loxP system produces a

CC reaction biased toward an irreversible gene inversion. The method of the
 CC invention facilitates investigation of the function of individual genes
 CC by a rapid extension of the conditional knockout approach

XX Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 13; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
 DB 34 TACCGTTCGTATA 22

RESULT 15

ABN84176/c
 ID ABN84176 standard; DNA; 34 BP.

XX AC

XX 19-FEB-2002 (first entry)

XX DE Synthetic lox66 sequence.

XX lox66; gene therapy; gene targeting; gene trapping;
 KW antisense RNA production; ds.

XX Synthetic.

XX WO200185973-A1.

XX 15-NOV-2001.

XX 29-AUG-2000; 2000WO-JP005824.

XX 11-MAY-2000; 2000JP-00138938.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Taniguchi M, Karasawa M;

XX WPI; 2002-055602/07.

XX Antisense type gene trap vector, useful for gene therapy of diseases and
 PT production of animal models for disease study, disrupts transcription of
 PT specific gene.

XX Claim 19; Page 43; 48pp; Japanese.

XX The invention relates to a method for producing cells in which the
 CC expression of a gene is disrupted. The cells are transformed with a gene
 CC trap vector to give a trap clone having the vector inserted at a specific
 CC mutation site of the target gene. The trap clone is then transformed with
 CC a vector that inserts a promoter in the antisense direction of the gene,
 CC enforcing transcription of antisense RNA. The method is useful for the
 CC production of animal models for studying human diseases. It is also
 CC useful as gene therapy for the treatment and prevention of diseases. The
 CC present sequence is a lox66 sequence claimed in the specification

XX Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 13; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
 DB 34 TACCGTTCGTATA 22

Search completed: December 24, 2004, 08:41:53
 Job time : 215 secs

us-10-030-658b-1.rng

Mon Dec 27 14:12:26 2004

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 08:14:39 ; Search time 49 Seconds
(without alignments)
188.577 Million cell updates/sec

Title: US-10-030-658B-1

Perfect score: 13

Sequence: 1 taccgttcgtata 13

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/1/ina/5A COMB.seq:*

2: /cgn2_6/prodata/1/ina/5B COMB.seq:*

3: /cgn2_6/prodata/1/ina/6A COMB.seq:*

4: /cgn2_6/prodata/1/ina/6B COMB.seq:*

5: /cgn2_6/prodata/1/ina/PCTUS COMB.seq:*

6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	92.3	606	4	US-09-270-767-7235, Ap
2	12	92.3	606	4	US-09-270-767-22517, A
3	12	92.3	630	4	US-09-270-767-10568, A
4	12	92.3	960	4	US-09-328-352-580, App
5	12	92.3	2142	4	US-09-614-221A-331, App
6	11.4	87.7	249	4	US-09-107-532A-1707, App
7	11.4	87.7	261	1	US-08-307-499-39, Appl
8	11.4	87.7	261	3	US-09-299-268-39, Appl
9	11.4	87.7	285	1	US-07-675-772-6, Appl
10	11.4	87.7	293	4	US-09-313-294A-1338, App
11	11.4	87.7	351	4	US-09-614-221A-215, App
12	11.4	87.7	384	5	PCT-US96-04648-5, Appl
13	11.4	87.7	437	4	US-09-270-767-7147, App
14	11.4	87.7	437	4	US-09-270-767-22429, A
15	11.4	87.7	498	4	US-09-489-039A-6859, App
16	11.4	87.7	702	4	US-09-270-767-9448, App
17	11.4	87.7	702	4	US-09-270-767-24730, A
18	11.4	87.7	705	1	US-08-178-242-7, Appl
19	11.4	87.7	705	2	US-08-955-091-7, Appl
20	11.4	87.7	705	3	US-09-225-510-7, Appl
21	11.4	87.7	715	4	US-09-270-767-10243, A
22	11.4	87.7	741	3	US-08-998-416-953, Appl
23	11.4	87.7	751	4	US-09-687-698-1, Appl
24	11.4	87.7	751	4	US-09-705-621-17, Appl
25	11.4	87.7	758	2	US-08-720-258-1, Appl
26	11.4	87.7	801	4	US-09-248-796A-3243, App
27	11.4	87.7	831	4	US-09-489-039A-2499, App

C 28	11.4	87.7	900	4	US-09-107-532A-2327	Sequence 2327, Ap
C 29	11.4	87.7	1016	1	US-08-178-242-5	Sequence 5, Appli
C 30	11.4	87.7	1016	2	US-08-955-091-5	Sequence 5, Appli
C 31	11.4	87.7	1016	3	US-09-225-510-5	Sequence 5, Appli
C 32	11.4	87.7	1067	4	US-09-780-717-25	Sequence 25, Appl
C 33	11.4	87.7	1071	4	US-09-543-681A-2390	Sequence 2390, Ap
C 34	11.4	87.7	1076	1	US-08-178-242-6	Sequence 6, Appli
C 35	11.4	87.7	1076	2	US-08-955-091-6	Sequence 6, Appli
C 36	11.4	87.7	1076	3	US-09-225-510-6	Sequence 6, Appli
C 37	11.4	87.7	1083	4	US-09-614-912-119	Sequence 119, App
C 38	11.4	87.7	1090	4	US-09-270-767-2889	Sequence 2889, Ap
C 39	11.4	87.7	1090	4	US-09-270-767-18171	Sequence 18171, A
C 40	11.4	87.7	1092	4	US-09-489-039A-6864	Sequence 6864, Ap
C 41	11.4	87.7	1095	4	US-09-809-665A-150	Sequence 150, App
C 42	11.4	87.7	1100	4	US-09-614-912-109	Sequence 109, App
C 43	11.4	87.7	1101	4	US-09-248-796A-3238	Sequence 3238, Ap
C 44	11.4	87.7	1135	4	US-09-270-767-2705	Sequence 2705, Ap
C 45	11.4	87.7	1135	4	US-09-270-767-17987	Sequence 17987, A

ALIGNMENTS

RESULT 1

US-09-270-767-7235
; Sequence 7235, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7235
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-7235

Query Match 92.3%; Score 12; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TACCGTTCGTAT	12
Db	572	TACCGTTCGTAT	583

RESULT 2

US-09-270-767-22517
; Sequence 22517, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22517
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-22517

Query Match 92.3%; Score 12; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TACCGTTCGTAT	12
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us-10-030-658b-1.rni

Mon Dec 27 14:12:26 2004

NUMBER OF SEQ ID NOS: 626
 SEQ ID NO 331
 LENGTH: 2142
 TYPE: DNA
 ORGANISM: Saccharomyces cerevisiae
 US-09-614-221A-331

Query Match 92.3%; Score 12; DB 4; Length 2142;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTAT 12
 Db 1521 TACCGTTCGTAT 1532

RESULT 6

US-09-107-532A-1707/c
 Sequence 1707, Application US/09107532A
 Patent No. 6583275
 GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02354

COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
 NAME: Ariniello, Pamela Deneka
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 1707:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 249 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (8) LOCATION 1...249
 SEQUENCE DESCRIPTION: SEQ ID NO: 1707:

US-09-107-532A-1707

Query Match 87.7%; Score 11.4; DB 4; Length 249;
 Best Local Similarity 92.3%; Pred. No. 3.9e+02; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 572 TACCGTTCGTAT 583

RESULT 3

US-09-270-767-10568
 Sequence 10568, Application US/09270767
 Patent No. 6703491
 GENERAL INFORMATION:
 APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 FILE REFERENCE: File Reference: 7326-094
 CURRENT APPLICATION NUMBER: US/09/270,767
 CURRENT FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 62517
 SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10568
 LENGTH: 630
 TYPE: DNA

ORGANISM: Drosophila melanogaster
 US-09-270-767-10568

Query Match 92.3%; Score 12; DB 4; Length 630;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTAT 12
 Db 410 TACCGTTCGTAT 421

RESULT 4

US-09-328-352-580/c
 Sequence 580, Application US/09328352
 Patent No. 6562958
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO 580
 LENGTH: 960
 TYPE: DNA

ORGANISM: Acinetobacter baumannii
 US-09-328-352-580

Query Match 92.3%; Score 12; DB 4; Length 960;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTAT 12
 Db 184 TACCGTTCGTAT 173

RESULT 5

US-09-614-221A-331
 Sequence 331, Application US/09614221A
 Patent No. 6723837
 GENERAL INFORMATION:
 APPLICANT: Karunanandaa, Balasulojini

APPLICANT: Yu, Jaehyuk
 APPLICANT: Kishore, Ganesh M.
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
 WITH STEROL SYNTHESIS AND METABOLISM
 FILE REFERENCE: 16516.075
 CURRENT APPLICATION NUMBER: US/09/614,221A
 CURRENT FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/142,981
 PRIOR FILING DATE: 1999-07-12

Query Match 87.7%; Score 11.4; DB 4; Length 249;
 Best Local Similarity 92.3%; Pred. No. 3.9e+02; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
|||||
Db 175 TACCATTCGTATA 163

RESULT 7
US-08-307-499-39/c
; Sequence 39, Application US/08307499
; Patent No. 5651972
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Gibbs, E.P.J.
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
; TITLE OF INVENTION: Live Vaccine Vector
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,499
; FILING DATE:
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,241
; FILING DATE: 1-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,630
; FILING DATE: 29-JUN-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/342,212
; FILING DATE: 21-APR-1992

; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-307-499-39

Query Match 87.7%; Score 11.4; DB 1; Length 261;
; Best Local Similarity 92.3%; Pred. No. 3.9e+02;
; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
|||||
Db 235 TATCGTTCGTATA 223

RESULT 8
US-09-299-268-39/c
; Sequence 39, Application US/09299268
; Patent No. 6217882
; GENERAL INFORMATION:

; APPLICANT: Moyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Gibbs, E.P.J.
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
; TITLE OF INVENTION: Live Vaccine Vector
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,268
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/901,127
; FILING DATE:
; APPLICATION NUMBER: US 07/908,241
; FILING DATE: 1-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,630
; FILING DATE: 29-JUN-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/342,212
; FILING DATE: 21-APR-1992

; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-09-299-268-39

Query Match 87.7%; Score 11.4; DB 3; Length 261;
; Best Local Similarity 92.3%; Pred. No. 3.9e+02;
; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
|||||
Db 235 TATCGTTCGTATA 223

RESULT 9
US-07-675-772-6/c
; Sequence 6, Application US/07675772
; Patent No. 5262399
; GENERAL INFORMATION:

; APPLICANT: Hickie, Leslie A.
; APPLICANT: Sick, August J.
; APPLICANT: Schwab, George E.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Payne, Jewel M.
; TITLE OF INVENTION: No. 5262399el Compositions and Methods for the Control of
; TITLE OF INVENTION: Flukes
; NUMBER OF SEQUENCES: 6

RESULT 11
US-09-614-221A-215/c

RESULT 11
MS-09-614-221A-215/c

QY 1 TACCGTTCGIATA 13

[illegible]

1 13

Db 110 TACCGTTCGTAGA 122
|||||||

RESULT 13

US-09-270-767-7147
; Sequence 7147, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7147
; LENGTH: 437
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-7147

Query Match 87.7%; Score 11.4; DB 4; Length 437;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
|||||||
Db 16 TACAGTTCGTATA 28

RESULT 14

US-09-270-767-22429
; Sequence 22429, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22429
; LENGTH: 437
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-22429

Query Match 87.7%; Score 11.4; DB 4; Length 437;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
|||||||
Db 16 TACAGTTCGTATA 28

RESULT 15

US-09-489-039A-6859/c
; Sequence 6859, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6859

; LENGTH: 498
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6859

Query Match 87.7%; Score 11.4; DB 4; Length 498;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
|||||||
Db 130 TACCGTTCGTATA 118

Search completed: December 24, 2004, 10:12:53
Job time : 51 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 09:10:55 ; Search time 221.5 Seconds
(without alignments)
326.801 Million cell updates/sec

Title: US-10-030-658B-1
Perfect score: 13
Sequence: 1 taccgttcgtata 13

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4105333 seqs, 2784095677 residues

Total number of hits satisfying chosen parameters: 8210666

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
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10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
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16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	33	14	US-10-118-231-1
2	13	100.0	33	14	US-10-118-231-2
3	13	100.0	34	10	US-09-957-660-2
4	13	100.0	34	10	US-09-957-660-3
5	13	100.0	34	10	US-09-957-660-4
6	13	100.0	34	10	US-09-957-660-4
7	13	100.0	34	14	US-10-118-231-18
8	13	100.0	34	14	US-10-118-231-1
9	13	100.0	34	14	US-10-214-722-6
10	13	100.0	34	14	US-10-214-722-8
11	13	100.0	34	16	US-10-416-995-9
12	13	100.0	34	16	US-10-416-995-10

c	13	100.0	34	17	US-10-739-769-2	Sequence 2, Appli
c	14	100.0	34	17	US-10-739-769-3	Sequence 3, Appli
c	15	100.0	34	17	US-10-739-769-4	Sequence 4, Appli
c	16	100.0	34	17	US-10-739-769-4	Sequence 4, Appli
c	17	100.0	34	17	US-10-739-769-5	Sequence 5, Appli
c	18	100.0	34	17	US-10-739-769-6	Sequence 6, Appli
c	19	100.0	34	18	US-10-448-395-2	Sequence 2, Appli
c	20	100.0	34	18	US-10-448-395-8	Sequence 8, Appli
c	21	100.0	34	18	US-10-448-395-13	Sequence 13, Appli
c	22	100.0	34	18	US-10-448-395-14	Sequence 14, Appli
c	23	100.0	40	10	US-09-899-615-4	Sequence 4, Appli
c	24	100.0	40	18	US-10-448-395-15	Sequence 15, Appli
c	25	100.0	40	18	US-10-448-395-16	Sequence 16, Appli
c	26	100.0	40	18	US-10-448-395-17	Sequence 17, Appli
c	27	100.0	40	18	US-10-448-395-18	Sequence 18, Appli
c	28	100.0	44	14	US-10-214-722-14	Sequence 14, Appli
c	29	100.0	44	14	US-10-214-722-15	Sequence 15, Appli
c	30	100.0	67	14	US-10-214-722-12	Sequence 12, Appli
c	31	100.0	68	14	US-10-214-722-11	Sequence 11, Appli
c	32	100.0	94	14	US-10-118-231-10	Sequence 10, Appli
c	33	100.0	94	14	US-10-118-231-10	Sequence 10, Appli
c	34	100.0	94	14	US-10-118-231-16	Sequence 16, Appli
c	35	100.0	94	14	US-10-118-231-16	Sequence 16, Appli
c	36	100.0	485	16	US-10-424-599-20024	Sequence 2024, A
c	37	100.0	489	18	US-10-425-115-178519	Sequence 178519, A
c	38	100.0	507	16	US-10-425-114-2962	Sequence 2962, Ap
c	39	100.0	951	9	US-09-727-855B-3	Sequence 3, Appli
c	40	100.0	1512	9	US-09-938-842A-801	Sequence 801, App
c	41	100.0	1512	11	US-09-938-842A-801	Sequence 801, App
c	42	100.0	2133	18	US-10-448-395-1	Sequence 1, Appli
c	43	100.0	242	16	US-10-424-599-139159	Sequence 139159, A
c	44	92.3	287	18	US-10-425-115-110479	Sequence 110479, A
c	45	92.3	491	17	US-10-437-963-17515	Sequence 17515, A

ALIGNMENTS

RESULT 1
US-10-118-231-1
; Sequence 1, Application US/10118231
; Publication NO. US20030005478A1
; GENERAL INFORMATION:
; APPLICANT: Bigger, Brian W
; APPLICANT: Tolmachov, Oleg
; APPLICANT: Coutelle, Charles
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 102286.141US
; CURRENT APPLICATION NUMBER: US/10/118,231
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/327,029
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: GB 0108968.9
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: left element
; OTHER INFORMATION: (LE) loxp site (also known as lox71)
US-10-118-231-1

Query Match 100.0%; Score 13; DB 14; Length 33;
Best Local Similarity 100.0%; Pred. NO. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13

DB 1 TACCGTTCGTATA 13

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RESULT 2
US-10-118-231-2/c
; Sequence 2, Application US/10118231
; Publication No. US20030005478A1
; GENERAL INFORMATION:
; APPLICANT: Bigger, Brian W
; APPLICANT: Tolmachov, Oleg
; APPLICANT: Coutelle, Charles
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 102286.141US
; CURRENT APPLICATION NUMBER: US/10/118,231
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/327,029
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: GB 0108968.9
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: right element
; OTHER INFORMATION: (RE) loxp site (also known as lox66)
US-10-118-231-2
Query Match 100.0%; Score 13; DB 14; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATA 13
Db 33 TACCGTTCGTATA 21

RESULT 3
US-09-957-660-2/c
; Sequence 2, Application US/09957660
; Publication No. US20030100077A1
; GENERAL INFORMATION:
; APPLICANT: KORTE, JOHN A.
; TITLE OF INVENTION: IN VITRO METHOD TO CREATE CIRCULAR MOLECULES FOR USE IN
; TITLE OF INVENTION: TRANSFORMATION
; FILE REFERENCE: DEKM:176US
; CURRENT APPLICATION NUMBER: US/09/957,660
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-957-660-2
Query Match 100.0%; Score 13; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATA 13
Db 34 TACCGTTCGTATA 22

RESULT 4
US-09-957-660-3
; Sequence 3, Application US/09957660
; Publication No. US20030100077A1
; GENERAL INFORMATION:
; APPLICANT: KORTE, JOHN A.
; TITLE OF INVENTION: IN VITRO METHOD TO CREATE CIRCULAR MOLECULES FOR USE IN
; TITLE OF INVENTION: TRANSFORMATION
; FILE REFERENCE: DEKM:176US
; CURRENT APPLICATION NUMBER: US/09/957,660
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-957-660-3
Query Match 100.0%; Score 13; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATA 13
Db 1 TACCGTTCGTATA 13

RESULT 5
US-09-957-660-4
; Sequence 4, Application US/09957660
; Publication No. US20030100077A1
; GENERAL INFORMATION:
; APPLICANT: KORTE, JOHN A.
; TITLE OF INVENTION: IN VITRO METHOD TO CREATE CIRCULAR MOLECULES FOR USE IN
; TITLE OF INVENTION: TRANSFORMATION
; FILE REFERENCE: DEKM:176US
; CURRENT APPLICATION NUMBER: US/09/957,660
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-957-660-4
Query Match 100.0%; Score 13; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATA 13
Db 1 TACCGTTCGTATA 13

RESULT 6
US-09-957-660-4/c
; Sequence 4, Application US/09957660
; Publication No. US20030100077A1
; GENERAL INFORMATION:
; APPLICANT: KORTE, JOHN A.
; TITLE OF INVENTION: IN VITRO METHOD TO CREATE CIRCULAR MOLECULES FOR USE IN
; TITLE OF INVENTION: TRANSFORMATION
; FILE REFERENCE: DEKM:176US
; CURRENT APPLICATION NUMBER: US/09/957,660
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-957-660-4/c
Query Match 100.0%; Score 13; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATA 13
Db 1 TACCGTTCGTATA 13
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-957-660-4

Query Match      100.0%; Score 13; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCGTTCGTATA 13
Db      34 TACCGTTCGTATA 22

RESULT 7
US-10-118-231-18/c
; Sequence 18, Application US/10118231
; Publication No. US2003005478A1
; GENERAL INFORMATION:
; APPLICANT: Bigger, Brian W
; APPLICANT: Tolmachov, Oleg
; APPLICANT: Coutelle, Charles
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 102286.141US
; CURRENT APPLICATION NUMBER: US/10/118,231
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/327,029
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: GB 0108968.9
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Construct
US-10-118-231-18

Query Match      100.0%; Score 13; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCGTTCGTATA 13
Db      34 TACCGTTCGTATA 22

RESULT 8
US-10-214-722-1/c
; Sequence 1, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; TITLE OF INVENTION: consecutive recombination-mediated recombinations
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide lox 66 without flanks
US-10-214-722-1

Query Match      100.0%; Score 13; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCGTTCGTATA 13
Db      34 TACCGTTCGTATA 22

RESULT 9
US-10-214-722-6
; Sequence 6, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; TITLE OF INVENTION: consecutive recombination-mediated recombinations
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide lox 71 without flanks
US-10-214-722-6

Query Match      100.0%; Score 13; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCGTTCGTATA 13
Db      1 TACCGTTCGTATA 13

RESULT 10
US-10-214-722-8
; Sequence 8, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; TITLE OF INVENTION: consecutive recombination-mediated recombinations
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-214-722-8
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Query Match 100.0%; Score 13; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0;

QY 1 TACCGTTCGTATA 13
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Db 1 TACCGTTCGTATA 13

RESULT 11
US-10-416-995-9/c
; Sequence 9, Application US/10416995
; Publication No. US20040077089A1
; GENERAL INFORMATION:
; APPLICANT: Xin, Hong-Bo
; APPLICANT: Kotlikoff, Michael
; TITLE OF INVENTION: CORNELL RESEARCH FOUNDATION, INC.
; TITLE OF INVENTION: VECTORS FOR CONDITIONAL GENE INACTIVATION
; FILE REFERENCE: 1153.020US1
; CURRENT APPLICATION NUMBER: US/10/416,995
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: PCT/US01/43916
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,200
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A mutant loxp sequence
US-10-416-995-9

Query Match 100.0%; Score 13; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0;

QY 1 TACCGTTCGTATA 13
|||
Db 34 TACCGTTCGTATA 22

RESULT 12
US-10-416-995-10/c
; Sequence 10, Application US/10416995
; Publication No. US20040077089A1
; GENERAL INFORMATION:
; APPLICANT: Xin, Hong-Bo
; APPLICANT: Kotlikoff, Michael
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: VECTORS FOR CONDITIONAL GENE INACTIVATION
; FILE REFERENCE: 1153.020US1
; CURRENT APPLICATION NUMBER: US/10/416,995
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: PCT/US01/43916
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,200
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A mutant loxp sequence
US-10-416-995-10

Query Match 100.0%; Score 13; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
|||
Db 34 TACCGTTCGTATA 22

RESULT 13
US-10-739-769-2/c
; Sequence 2, Application US/10739769
; Publication No. US20040137624A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; TITLE OF INVENTION: Methods of Site-Directed Transformation
; FILE REFERENCE: 38-15(52823)B
; CURRENT APPLICATION NUMBER: US/10/739,769
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: variant of wild type loxp recombinase site
US-10-739-769-2

Query Match 100.0%; Score 13; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0;

QY 1 TACCGTTCGTATA 13
|||
Db 34 TACCGTTCGTATA 22

RESULT 14
US-10-739-769-3
; Sequence 3, Application US/10739769
; Publication No. US20040137624A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; TITLE OF INVENTION: Methods of Site-Directed Transformation
; FILE REFERENCE: 38-15(52823)B
; CURRENT APPLICATION NUMBER: US/10/739,769
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: variant of wild-type loxp recombination site
US-10-739-769-3

Query Match 100.0%; Score 13; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0;

QY 1 TACCGTTCGTATA 13
|||
Db 1 TACCGTTCGTATA 13

RESULT 15
US-10-739-769-4
; Sequence 4, Application US/10739769
; Publication No. US20040137624A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; TITLE OF INVENTION: Methods of Site-Directed Transformation
; FILE REFERENCE: 38-15(52823)B

;
; CURRENT APPLICATION NUMBER: US/10/739,769
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: variant of wild-type loxP recombination site
US-10-739-769-4

Query Match 100.0%; Score 13; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATA 13
|||
Db 1 TACCGTTCGTATA 13

Search completed: December 24, 2004, 11:42:14
Job time : 222.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 08:02:10 ; Search time 1774.5 Seconds
(without alignments)
266.958 Million cell updates/sec

Title: US-10-030-658B-1

Perfect score: 13

Sequence: 1 taccgttcgtata 13

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_gseq1:*

9: gb_gseq2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13	100.0	233	8	BH855321
C 2	13	100.0	288	2	AW927382
C 3	13	100.0	308	2	AW927383
C 4	13	100.0	313	5	AJ592954
C 5	13	100.0	367	5	BM964186
C 6	13	100.0	438	8	AQ711712
C 7	13	100.0	468	8	AQ650435
C 8	13	100.0	498	8	AQ204576
C 9	13	100.0	498	2	AW682787
C 10	13	100.0	504	9	CL734978
C 11	13	100.0	505	6	CB408882
C 12	13	100.0	534	4	BI455837
C 13	13	100.0	539	4	BM899392
C 14	13	100.0	553	9	CL598552
C 15	13	100.0	595	8	AQ574962
C 16	13	100.0	606	5	BQ380889
C 17	13	100.0	619	8	AQ649203
C 18	13	100.0	668	8	BH945623
C 19	13	100.0	669	8	AQ498235
C 20	13	100.0	708	9	CL599162
C 21	13	100.0	709	7	CF817293
C 22	13	100.0	761	5	BW455623
C 23	13	100.0	806	9	AG098437
C 24	13	100.0	896	9	AG508374

C 25	13	100.0	900	4	BG400144
C 26	13	100.0	915	7	CF548337
C 27	13	100.0	924	6	CB561239
C 28	13	100.0	982	9	CNS06H7X
C 29	13	100.0	1020	9	CNS0006D9
C 30	13	100.0	1118	9	AG511186
C 31	13	100.0	1286	5	BU326180
C 32	13	100.0	2306	9	CL511272
C 33	13	100.0	2945	7	CO760796
C 34	13	100.0	2945	7	CO760796
C 35	12	92.3	124	5	BM966340
C 36	12	92.3	131	9	CC882306
C 37	12	92.3	167	8	EX948525
C 38	12	92.3	167	8	CC104285
C 39	12	92.3	171	2	BB052078
C 40	12	92.3	185	8	BH896578
C 41	12	92.3	206	1	AV363052
C 42	12	92.3	229	8	AQ473103
C 43	12	92.3	237	2	BE525828
C 44	12	92.3	237	3	CNS08GBR
C 45	12	92.3	242	5	BW042380
C 45	12	92.3	250	7	CN800693

ALIGNMENTS

BH855321 233 bp DNA linear GSS 08-JUL-2002
SALK_085977.20.05.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_085977.20.05.x, genomic
survey sequence.

BH855321 GI:21704911

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL

COMMENT

Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
TDNA.

Class: TDNA tagged.

FEATURES

source

Location/Qualifiers
1..233
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_085977.20.05.x"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

AG508374 Mus muscu

```

Query Match      100.0%; Score 13; DB 8; Length 233;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
   |||||
Db 121 TACCGTTCGTATA 109

RESULT 2
AW927382/c
LOCUS      945017D12.X1 945 - Mixed adult tissues from Walbot lab, same as 707
DEFINITION (SK) Zea mays cDNA, mRNA sequence.
ACCESSION  AW927382
VERSION     AW927382
KEYWORDS    EST.
SOURCE      AW927382.1 GI:8102741
ORGANISM    Zea mays
            Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 288)
AUTHORS    Walbot,V.
TITLE      Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL     University
COMMENT     Unpublished (1999)
            Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 945017 row: D column: 12.
            Location/Qualifiers
                1..288
                /organism="Zea mays"
                /mol_type="mRNA"
                /cultivar="W23"
                /db_xref="taxon:4577"
                /tissue_type="tassel, kernal, silk, husk, root, leaf"
                /dev_stage="fully-grown"
                /lab_host="DH10B"
                /clone_lib="945 - Mixed adult tissues from Walbot lab,
                same as 707 (SK)"
                /note="Organ: tassel, kernal, silk, husk, root, leaf;
                Vector: pGAD10; Site 1: EcoRI; cDNA library from fully
                differentiated maize tissues from an active Mutator plant.
                Tissue ratio is 4:2:1:1:1 (tassel, kernal, silk, husk,
                root, leaf). Unidirectionally cloned. New library number
                given to library 707 for additional sequencing."

FEATURES             source
            Location/Qualifiers
            1..288
            /organism="Zea mays"
            /mol_type="mRNA"
            /cultivar="W23"
            /db_xref="taxon:4577"
            /tissue_type="tassel, kernal, silk, husk, root, leaf"
            /dev_stage="fully-grown"
            /lab_host="DH10B"
            /clone_lib="945 - Mixed adult tissues from Walbot lab,
            same as 707 (SK)"
            /note="Organ: tassel, kernal, silk, husk, root, leaf;
            Vector: pGAD10; Site 1: EcoRI; cDNA library from fully
            differentiated maize tissues from an active Mutator plant.
            Tissue ratio is 4:2:1:1:1 (tassel, kernal, silk, husk,
            root, leaf). Unidirectionally cloned. New library number
            given to library 707 for additional sequencing."

ORIGIN
Query Match      100.0%; Score 13; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
   |||||
Db 40 TACCGTTCGTATA 28

RESULT 4
AW592954
LOCUS      Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 372D03, genomic survey sequence.
ACCESSION  AJ592954
VERSION     AJ592954.1 GI:37942578
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE   1
AUTHORS    Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE      T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
JOURNAL     EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE     22363535
PUBMED      12446565
REFERENCE   2 (bases 1 to 313)
AUTHORS    Balzerque,S.
TITLE      Direct Submission
JOURNAL     Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from

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the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.veraillies.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES

source
1. .313
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="372003"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature
1. .313
/notes="T-DNA flanking sequence
left border"

ORIGIN

Query Match 100.0%; Score 13; DB 9; Length 313;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13

Db 36 TACCGTTCGTATA 48

RESULT 5

BM964186/c

LOCUS

DEFINITION BM964186 367 bp mRNA linear EST 18-MAR-2002
UI-M-EQO-bvu-m-01-0-UI.r1 NIH-BMAP_EQO Mus musculus cDNA clone
IMAGE:5697192 5', mRNA sequence.

ACCESSION

BM964186

VERSION

BM964186.1

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 367)

REFERENCE

NIH-MGC <http://mgc.nci.nih.gov/>

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgaps-x@mail.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

<http://image.lnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pyx-5.

Location/Qualifiers

1. .367

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:5697192"

/tissue_type="whole brain"

/dev_stage="embryo 15.5 dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH-BMAP_EQO"

/note="Organ: brain; Vector: pyx-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCACGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 100.0%; Score 13; DB 5; Length 367;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13

Db 274 TACCGTTCGTATA 262

RESULT 6

AQ711712

LOCUS

DEFINITION

HS 5376 B1 F05 SP6E RPCI-11 Human Male BAC library Homo sapiens

genomic_clone Plate=952 Col=9 Row=L, genomic survey sequence.

AQ711712

ACCESSION

AQ711712.1

VERSION

GI:5461028

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 438)

REFERENCE

MAHAIAS, G.G., WALLACE, J.C., SMITH, K., SWARTZELL, S., HOLZMAN, T.,

KELLER, A., SHAKER, R., FURLONG, J., YOUNG, J., ZHAC, S., ADAMS, M.D. and

HOOD, L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

99380589

MEDLINE

10449764

PUBMED

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/bac.htm>)

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

<http://www.htac.washington.edu>

Plate: 952 row: L column: 9

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 438.

Location/Qualifiers

1. .438

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=952 Col=9 Row=L"

/sex="male"

/clone_lib="RPCI-11 Human Male BAC Library"

/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the

pBACE3.6 vector at EcoRI sites"

ORIGIN

Query Match 100.0%; Score 13; DB 8; Length 438;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
 |||||
 Db 123 TACCGTTCGTATA 135

RESULT 7

AQ650435/c
 LOCUS
 DEFINITION Sheared DNA-18F1.TF Sheared DNA Trypanosoma brucei genomic clone
 Sheared DNA-18F1, genomic survey sequence.

ACCESSION AQ650435.1 GI:5143621
 VERSION
 KEYWORDS GSS.

SOURCE

ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE

AUTHORS El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
 Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S.,
 Donelson,J., Fraser,C. and Adams,M.
 Determination of clone end sequences from Trypanosoma brucei GUTat
 10.1 sheared DNA library
 Unpublished (1999)

JOURNAL

COMMENT Other_GSSs: Sheared DNA-18F1.TR

Contact: Najib M. El-Sayed
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208

Email: nelsayed@tigr.org
 Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
 DNA library constructed at TIGR. Clones will be available for
 distribution through ATCC. Sheared DNA end sequences search page:
<http://www.tigr.org/tdb/mdb/tbdb/>.

Seq primer: M13-Forward

Class: shotgun.

FEATURES

source

1..468
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927/4 GUTat 10.1"
 /db_xref="taxon:5691"
 /clone="Sheared DNA-18F1"
 /clone_lib="Sheared DNA"
 /notes="Vector: pUC18; Site 1: SmaI; Constructed at The
 Institute for Genomic Research (TIGR), Rockville, MD.
 Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
 sheared to give a tight size distribution (approx 2 kb).
 The v + i method used for the library construction is
 described in detail in Smith, H.O. and Venter, J.C.
 (Making small insert libraries for whole genome shotgun
 sequencing projects. In Genome Sequencing: A Practical
 Approach, eds. M. Vaudin and B. Borell, Oxford University
 Press, 1999)."

ORIGIN

Query Match 100.0%; Score 13; DB 8; Length 468;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
 |||||
 Db 96 TACCGTTCGTATA 84

RESULT 8

AQ204576
 LOCUS

DEFINITION

HS 3229 Bi B09 T7 CIT Approved Human Genomic Sperm Library D Homo
 sapiens_genomic clone Plate=3229 Col=17 Row=D, genomic survey
 sequence.

ACCESSION AQ204576
 VERSION AQ204576.1 GI:3615146
 KEYWORDS GSS.

SOURCE

ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 490)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Sequence Tagged Connector

Plate: 3229 Row: D Column: 17

Class: BAC ends

High quality sequence stop: 490.

Location/Qualifiers

1..490

source

/organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=3229 Col=17 Row=D"
 /sex="male"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
 E-Coli DH10B"

ORIGIN

Query Match 100.0%; Score 13; DB 8; Length 490;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13

Db 17 TACCGTTCGTATA 29

RESULT 9

LOCUS

AW682787/c
 DEFINITION
 (SAW99MLW-BmyD25) Brugia malayi young adult day 25 cDNA
 sequence.

ACCESSION AW682787
 VERSION AW682787.1 GI:7557489
 KEYWORDS EST.

SOURCE

ORGANISM

Brugia malayi
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 Onchocercidae; Brugia.
 1 (bases 1 to 498)

REFERENCE

AUTHORS

TITLE

JOURNAL

Genes expressed in young adult day 25 of Brugia malayi
 Unpublished (1999)

COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.

FEATURES
source
1. .498
/organism="Brugia malayi"
/mol_type="mRNA"
/db_xref="taxon:6279"
/clone="SWYD25CAU13A03"
/dev_stage="young adult, twenty five days after infection"
/lab_host="XLI-Blue MRF,"
/clone_lib="Brugia malayi young adult day 25 cDNA
(SAW99MLW-BmyD25)"
/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:
Xho I; Lymphatic filarial nematode parasite of humans.
mRNA was prepared from young adult worms isolated from
the peritoneal cavity of jirds on day 25 after infection
and converted to double-stranded cDNA using reverse
transcriptase and oligo(dT) followed by RNase H and DNA
pol I. The library has 6.2 x 105 independent recombinants
and the average insert size is approx. 1101bp. The library
was constructed by Michelle Lizotte-Waniewski. The
library is available from Dr. S.A. Williams, email:
genome@neal.smith.edu."

ORIGIN
Query Match 100.0%; Score 13; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
|||||
Db 184 TACCGTTCGTATA 172

RESULT 10
CL734978/c
LOCUS
DEFINITION CL734978 504 bp DNA linear GSS 27-JUL-2004
OR BBA0068P22.r OR BBA Oryza rufipogon genomic clone OR_BBA0068P22
3', genomic survey sequence.

ACCESSION
VERSION CL734978
KEYWORDS
SOURCE GSS.
CL734978.1 GI:50669334

ORGANISM
Oryza rufipogon
Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 504)
Kim.H., Yu.Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu

PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert length: 161 Std Error: 0.00
Plate: 0068 row: F column: 22
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source
1. .504
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_BBA0068P22"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBA"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match 100.0%; Score 13; DB 9; Length 504;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13
|||||
Db 68 TACCGTTCGTATA 56

RESULT 11
CB408882
LOCUS
DEFINITION CB408882 505 bp mRNA linear EST 24-OCT-2003
IPG018D06.250666 JH III-treated male I. pini midguts Ips pini cDNA
clone IPG018D06 5, mRNA sequence.

ACCESSION
VERSION CB408882
KEYWORDS
SOURCE EST.
CB408882.1 GI:37953018

ORGANISM
Ips pini (North American pine engraver)
Ips pini
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Scolytidae; Ips.
1 (bases 1 to 505)
Eigenheer,A.L., Keeling,C.I., Young,S. and Tittiger,C.
Comparison of gene representation in midguts from two phytophagous
insects, Bombyx mori and Ips pini, using expressed sequence tags
Gene 316, 127-136 (2003)
22925480
14563559
Contact: Tittiger C
Biochemistry Department
University of Nevada, Reno
Howard Medical Sciences Rm. 150, Reno, NV 89557, USA
Tel: 1-775-784-6480
Fax: 1-775-784-1419
Email: crt@unr.edu
PCR Primers
FORWARD: T7 21mer (backward)
BACKWARD: T3 21mer
Plate: 018 row: D column: 06
Seq primer: T3 21mer
High quality sequence stop: 505.

FEATURES
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1. .505
/organism="Ips pini"
/mol_type="mRNA"
/db_xref="taxon:102803"
/clone="IPG018D06"
/sex="male"
/tissue_type="midgut"
/dev_stage="adult"
/clone_lib="JH III-treated male I. pini midguts"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK; As per
Stratagene's pBluescript II XR library construction kit"

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Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13

FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Insert Length: 145000 Std Error: 0.00
 Plate: 0060 row: 0 column: 09
 Seq primer: TAA TAC GAC TCA CTA TAG GG
 Class: BAC ends.

FEATURES

source

Location/Qualifiers

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 /organism="Oryza brachyantha"
 /mol_type="genomic DNA"
 /db_xref="taxon:4533"
 /clone="OB_Ba0060009"
 /tissue_type="leaves"
 /dev_stage="mature"
 /lab_host="DH10B"
 /clone_lib="OB_Ba"
 /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13

|||||
 Db 517 TACCGTTCGTATA 529

RESULT 15

AQ574962/C

LOCUS

AQ574962

DEFINITION

nbxb0086B17f CUGI Rice BAC Library Oryza sativa (japonica
 cultivar-group) genomic clone nbxb0086B17f, genomic survey

ACCESSION

AQ574962

VERSION

AQ574962.1

KEYWORDS

GSS.

SOURCE

Oryza sativa

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 595)

Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome

Unpublished (1998)

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: TAATACGACTCACTATAGGG

Class: BAC ends

High quality sequence stop: 201.

FEATURES

source

Location/Qualifiers

1..595
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="genomic DNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="nbxb0086B17f"
 /tissue_type="leaf"
 /lab_host="E. coli DH10B"
 /clone_lib="CUGI Rice BAC Library"
 /note="Vector: pBelOBAC1; Site 1: HindIII; Site 2:
 HindIII; Rice is one of two most popular grains in the
 world. Half of the world population especially those
 inhabiting highly populated areas of the humid tropics
 and subtropics, rely on rice as their primary source of
 carbohydrate. Monocotyledonous rice is a diploid plant
 (2n=24) with a haploid genome equivalent of 431 Mbp

(Arumuganathan and Earle, 1991). The relatively small
 genome of rice, three times larger than that of
 Arabidopsis, makes it suitable for genomic studies. In
 order to facilitate positional cloning, physical mapping
 and genome sequencing of rice, we have constructed a BAC
 library from Oryza sativa, Nipponbare variety. The
 library contains 36,864 clones with an average insert size
 of 128.5 Kb providing 10.9 haploid genome equivalents. The
 deep coverage allows the isolation a particular sequence
 with a probability of 99.9 %. Two high density filters,
 each containing 19,432 clones (doubly spotted), represent
 the whole library for colony screening."

ORIGIN

Query Match 100.0%; Score 13; DB 8; Length 595;

Best Local Similarity 100.0%; Pred. No. 5.9e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATA 13

|||||
 Db 68 TACCGTTCGTATA 56

Search completed: December 24, 2004, 10:11:14

Job time : 1782.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 05:35:57 ; Search time 864.5 Seconds
(without alignments)
711.123 Million cell updates/sec

Title: US-10-030-658B-2
Perfect score: 13
Sequence: 1 tatacgaacggta 13

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13	100.0	13	6 BD091727	BD091727 Trap vect
C 2	13	100.0	13	6 BD091728	BD091728 Trap vect
C 3	13	100.0	33	6 AX662245	AX662245 Sequence
C 4	13	100.0	33	6 AX662246	AX662246 Sequence
C 5	13	100.0	34	6 BD182868	BD182868 Knockout
C 6	13	100.0	34	6 BD182869	BD182869 Knockout
C 7	13	100.0	34	6 BD182873	BD182873 Knockout
C 8	13	100.0	34	6 BD182873	BD182873 Knockout
C 9	13	100.0	34	6 BD185622	BD185622 Knockout
C 10	13	100.0	34	6 BD185623	BD185623 Knockout
C 11	13	100.0	34	6 BD185627	BD185627 Knockout
C 12	13	100.0	34	6 AX114842	AX114842 Sequence
C 13	13	100.0	34	6 AX114843	AX114843 Sequence
C 14	13	100.0	34	6 AX114843	AX114843 Sequence
C 15	13	100.0	34	6 AX114844	AX114844 Sequence
C 16	13	100.0	34	6 AX114844	AX114844 Sequence
C 17	13	100.0	34	6 AX137068	AX137068 Sequence
C 18	13	100.0	34	6 AX137069	AX137069 Sequence
C 19	13	100.0	34	6 AX137070	AX137070 Sequence

C 20	13	100.0	34	6 AX137070	AX137070 Sequence
C 21	13	100.0	34	6 AX540640	AX540640 Sequence
C 22	13	100.0	34	6 AX540641	AX540641 Sequence
C 23	13	100.0	34	6 AX710004	AX710004 Sequence
C 24	13	100.0	34	6 AX710009	AX710009 Sequence
C 25	13	100.0	34	6 AX710011	AX710011 Sequence
C 26	13	100.0	34	6 BD083072	BD083072 Antisense
C 27	13	100.0	34	6 BD083073	BD083073 Antisense
C 28	13	100.0	34	6 BD091732	BD091732 Trap vect
C 29	13	100.0	34	6 BD091732	BD091732 Trap vect
C 30	13	100.0	34	6 BD093611	BD093611 Antisense
C 31	13	100.0	34	6 BD093612	BD093612 Antisense
C 32	13	100.0	44	6 AX148779	AX148779 Sequence
C 33	13	100.0	44	6 AX710017	AX710017 Sequence
C 34	13	100.0	44	6 AX710018	AX710018 Sequence
C 35	13	100.0	67	6 AX710015	AX710015 Sequence
C 36	13	100.0	68	6 AX710014	AX710014 Sequence
C 37	13	100.0	79	6 AX114851	AX114851 Sequence
C 38	13	100.0	79	6 AX114852	AX114852 Sequence
C 39	13	100.0	94	6 AX662254	AX662254 Sequence
C 40	13	100.0	94	6 AX662254	AX662254 Sequence
C 41	13	100.0	94	6 AX662260	AX662260 Sequence
C 42	13	100.0	94	6 AX662260	AX662260 Sequence
C 43	13	100.0	388	5 AF317206	AF317206 Astyanax
C 44	13	100.0	388	5 AF317207	AF317207 Astyanax
C 45	13	100.0	390	11 CR383976	CR383976 Arabidops

ALIGNMENTS

RESULT 1
BD091727/c
LOCUS BD091727 13 bp DNA linear PAT 27-AUG-2002
DEFINITION Trap vector and gene trapping method by using the same.
ACCESSION BD091727
VERSION BD091727.1 GI:22637338
KEYWORDS WO 0105987-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 13)
AUTHORS Yamamura, K. and Araki, K.
TITLE Trap vector and gene trapping method by using the same
JOURNAL Patent: WO 0105987-A 1 25-JAN-2001.
COMMENT KUMAMOTO TECHNOLOGIES FOUNDATION, KENICHI YAMAMURA, KIYI ARAKI
OS Artificial Sequence
PN WO 0105987-A/1
PF 02-MAY-2000 WO 2000JP002916
PR 14-JUL-1999 JP 99P 200997
PI KENICHI YAMAMURA, KIYI ARAKI
PC Cl2N15/85, A01K67/027
CC Description of Artificial Sequence: synthetic DNA FH Key
Location/Qualifiers

FEATURES
Source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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Query Match 100.0%; Score 13; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATACGAACGGTA 13
|||||
DB 13 TATACGAACGGTA 1

RESULT 2
BD091728

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LOCUS      BD091728                      13 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Trap vector and gene trapping method by using the same.
ACCESSION  BD091728
VERSION    BD091728.1  GI:22637339
KEYWORDS   WO 0105987-A/2.
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1 (bases 1 to 13)
AUTHORS    Yamamura,K. and Araki,K.
TITLE      Trap vector and gene trapping method by using the same
JOURNAL    Patent: WO 0105987-A 2 25-JAN-2001;
           KUMAMOTO TECHNOLIS FOUNDATION,KENICHI YAMAMURA,KIMI ARAKI
COMMENT    OS Artificial Sequence
           PN WO 0105987-A/2
           PD 25-JAN-2001
           PF 02-MAY-2000 WO 2000JP002916
           PR 14-JUL-1999 JP 99P 200997
           PI KENICHI YAMAMURA,KIMI ARAKI
           PC C12N15/85,A01K67/027
           CC Description of Artificial Sequence:synthetic DNA FH Key
           Location/Qualifiers
FEATURES   source
           1..13
           /organism="synthetic construct"
           /mol_type="genomic DNA"
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ORIGIN
Query Match      100.0%; Score 13; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
      |||||
Db      1 TATACGAACGGTA 13

RESULT 3
AX662245/c
LOCUS      AX662245                      33 bp      DNA      linear      PAT 22-MAR-2003
DEFINITION Sequence 1 from Patent WO02083889.
ACCESSION  AX662245
VERSION    AX662245.1  GI:29163144
KEYWORDS   Bigger,B.W., Tolmachov,O. and Coutelle,C.
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Bigger,B.W., Tolmachov,O. and Coutelle,C.
TITLE      Methods
JOURNAL    Patent: WO 02083889-A 1 24-OCT-2002;
           IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES   Location/Qualifiers
           1..33
           /organism="synthetic construct"
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           /db_xref="taxon:32630"
           /note="Left element Lox P site"
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Query Match      100.0%; Score 13; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
      |||||
Db      13 TATACGAACGGTA 1

RESULT 4
AX662246
LOCUS      AX662246                      33 bp      DNA      linear      PAT 22-MAR-2003

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DEFINITION Sequence 2 from Patent WO02083889.
ACCESSION  AX662246
VERSION    AX662246.1  GI:29163145
KEYWORDS   synthetic construct
SOURCE     synthetic construct
           artificial sequences.
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Bigger,B.W., Tolmachov,O. and Coutelle,C.
TITLE      Methods
JOURNAL    Patent: WO 02083889-A 2 24-OCT-2002;
           IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES   Location/Qualifiers
           1..33
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="Right element LoxP site"
ORIGIN
Query Match      100.0%; Score 13; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
      |||||
Db      21 TATACGAACGGTA 33

RESULT 5
BD182868/c
LOCUS      BD182868                      34 bp      DNA      linear      PAT 17-JUN-2003
DEFINITION Knockout animal.
ACCESSION  BD182868
VERSION    BD182868.1  GI:31875068
KEYWORDS   JP 2002345477-A/1.
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1 (bases 1 to 34)
AUTHORS    Ide,H., Yamamura,K. and Araki,K.
TITLE      Knockout animal
JOURNAL    Patent: JP 2002345477-A 1 03-DEC-2002;
           JAPAN SCIENCE AND TECHNOLOGY CORP,HIROYUKI IDE,KENICHI YAMAMURA,
           KIMI ARAKI
COMMENT    OS Artificial Sequence
           PN JP 2002345477-A/1
           PD 03-DEC-2002
           PF 25-MAY-2001 JP 2001157567
           PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
           PC C12N15/09,A01K67/027,C12N5/10,C12N15/00,C12N5/00 CC
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           Location/Qualifiers
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           /organism="Artificial Sequence".
           /organism="synthetic construct"
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FEATURES   source
           1..34
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           /mol_type="genomic DNA"
           /db_xref="taxon:32630"
ORIGIN
Query Match      100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
      |||||
Db      13 TATACGAACGGTA 1

RESULT 6
BD182869

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LOCUS       BD182869                               34 bp      DNA          linear      PAT 17-JUN-2003
DEFINITION   Knockout animal.
ACCESSION    BD182869
VERSION      BD182869.1 GI:31875069
KEYWORDS     JP 2002345477-A/2.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 34)
AUTHORS      Ide H., Yamamura,K. and Araki,K.
TITLE        Knockout animal
JOURNAL      Patent: JP 2002345477-A 2 03-DEC-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP,HIROYUKI IDE,KENICHI YAMAMURA,
              KIMI ARAKI
COMMENT      OS Artificial Sequence
              PN JP 2002345477-A/2
              PD 03-DEC-2002
              PF 25-MAY-2001 JP 2001157567
              PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
              PC C12N15/09,A01K67/027,C12N5/10,C12N5/00 CC
              Description of Artificial Sequence:synthetic DNA FH Key
              Location/Qualifiers
              FT source 1..34
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FEATURES             source
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                     /db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
        |||||
Db      22 TATACGAACGGTA 34

RESULT 7
BD182873
LOCUS       BD182873                               34 bp      DNA          linear      PAT 17-JUN-2003
DEFINITION   Knockout animal.
ACCESSION    BD182873
VERSION      BD182873.1 GI:31875073
KEYWORDS     JP 2002345477-A/6.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 34)
AUTHORS      Ide H., Yamamura,K. and Araki,K.
TITLE        Knockout animal
JOURNAL      Patent: JP 2002345477-A 6 03-DEC-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP,HIROYUKI IDE,KENICHI YAMAMURA,
              KIMI ARAKI
COMMENT      OS Artificial Sequence
              PN JP 2002345477-A/6
              PD 03-DEC-2002
              PF 25-MAY-2001 JP 2001157567
              PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
              PC C12N15/09,A01K67/027,C12N5/10,C12N5/00,C12N5/00 CC
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ORIGIN
Query Match      100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
        |||||
Db      22 TATACGAACGGTA 34

RESULT 8
BD182873/c
LOCUS       BD182873/c                             34 bp      DNA          linear      PAT 17-JUN-2003
DEFINITION   Knockout animal.
ACCESSION    BD182873
VERSION      BD182873.1 GI:31875073
KEYWORDS     JP 2002345477-A/6.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 34)
AUTHORS      Ide H., Yamamura,K. and Araki,K.
TITLE        Knockout animal
JOURNAL      Patent: JP 2002345477-A 6 03-DEC-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP,HIROYUKI IDE,KENICHI YAMAMURA,
              KIMI ARAKI
COMMENT      OS Artificial Sequence
              PN JP 2002345477-A/6
              PD 03-DEC-2002
              PF 25-MAY-2001 JP 2001157567
              PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
              PC C12N15/09,A01K67/027,C12N5/10,C12N5/00,C12N5/00 CC
              Description of Artificial Sequence:synthetic DNA FH Key
              Location/Qualifiers
              FT source 1..34
              FT /organism='Artificial Sequence'.

FEATURES             source
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                     /mol_type="genomic DNA"
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ORIGIN
Query Match      100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
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Db      22 TATACGAACGGTA 34

RESULT 9
BD185622/c
LOCUS       BD185622/c                             34 bp      DNA          linear      PAT 17-JUN-2003
DEFINITION   Knockout animal.
ACCESSION    BD185622
VERSION      BD185622.1 GI:31877822
KEYWORDS     JP 2002369689-A/1.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 34)
AUTHORS      Ide H., Yamamura,K. and Araki,K.
TITLE        Knockout animal
JOURNAL      Patent: JP 2002369689-A 1 24-DEC-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP,EU GENE LTD, PRESIDENT OF
              KUMAMOTO UNIVERSITY
COMMENT      OS Artificial Sequence
              PN JP 2002369689-A/1
              PD 24-DEC-2002
              PF 25-MAY-2001 JP 2001157568
              PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
              PC C12N15/09,A01K67/027,C12N5/10,C12N5/00,C12N5/00 CC
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Query Match      100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
        |||||
Db      22 TATACGAACGGTA 34

RESULT 8
BD182873/c
LOCUS       BD182873/c                             34 bp      DNA          linear      PAT 17-JUN-2003
DEFINITION   Knockout animal.
ACCESSION    BD182873
VERSION      BD182873.1 GI:31875073
KEYWORDS     JP 2002345477-A/6.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 34)
AUTHORS      Ide H., Yamamura,K. and Araki,K.
TITLE        Knockout animal
JOURNAL      Patent: JP 2002345477-A 6 03-DEC-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP,HIROYUKI IDE,KENICHI YAMAMURA,
              KIMI ARAKI
COMMENT      OS Artificial Sequence
              PN JP 2002345477-A/6
              PD 03-DEC-2002
              PF 25-MAY-2001 JP 2001157567
              PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
              PC C12N15/09,A01K67/027,C12N5/10,C12N5/00,C12N5/00 CC
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              Location/Qualifiers
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FEATURES             source
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Query Match      100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
        |||||
Db      13 TATACGAACGGTA 1

RESULT 9
BD185622/c
LOCUS       BD185622/c                             34 bp      DNA          linear      PAT 17-JUN-2003
DEFINITION   Knockout animal.
ACCESSION    BD185622
VERSION      BD185622.1 GI:31877822
KEYWORDS     JP 2002369689-A/1.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 34)
AUTHORS      Ide H., Yamamura,K. and Araki,K.
TITLE        Knockout animal
JOURNAL      Patent: JP 2002369689-A 1 24-DEC-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP,EU GENE LTD, PRESIDENT OF
              KUMAMOTO UNIVERSITY
COMMENT      OS Artificial Sequence
              PN JP 2002369689-A/1
              PD 24-DEC-2002
              PF 25-MAY-2001 JP 2001157568
              PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
              PC C12N15/09,A01K67/027,C12N5/10,C12N5/00,C12N5/00 CC
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Mon Dec 27 14:12:27 2004

us-10-030-658b-2.rge

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AUTHORS      Ide,H., Yamamura,K. and Araki,K.
TITLE        Knockout animal
JOURNAL      Patent: JP 2002369689-A 6 24-DEC-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP,EU GENE LTD, PRESIDENT OF
              KUMAMOTO UNIVERSITY
COMMENT      OS Artificial Sequence
              PN JP 2002369689-A/6
              PD 24-DEC-2002
              PF 25-MAY-2001 JP 2001157568
              PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
              PC C12N15/09,A01K67/027,C12N5/10,C12N15/00,C12N5/00 CC
              Description of Artificial Sequence:synthetic DNA FH Key
              Location/Qualifiers
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FEATURES
source
1..34
/organism="synthetic construct"
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Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13
   |||||
Db 22 TATACGAACGGTA 34

RESULT 12
BD185627/c
LOCUS      Knockout animal.
DEFINITION
ACCESSION  BD185627
VERSION     BD185627.1 GI:31877827
KEYWORDS   JP 2002369689-A/6.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE   1 (bases 1 to 34)
AUTHORS     Ide,H., Yamamura,K. and Araki,K.
TITLE       Knockout animal
JOURNAL     Patent: JP 2002369689-A 2 24-DEC-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP,EU GENE LTD, PRESIDENT OF
              KUMAMOTO UNIVERSITY
COMMENT     OS Artificial Sequence
              PN JP 2002369689-A/2
              PD 24-DEC-2002
              PF 25-MAY-2001 JP 2001157568
              PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
              PC C12N15/09,A01K67/027,C12N5/10,C12N15/00,C12N5/00 CC
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              Location/Qualifiers
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source
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/organism="synthetic construct"
/mol_type="genomic DNA"
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ORIGIN
Query Match 100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13
   |||||
Db 22 TATACGAACGGTA 34

RESULT 11
BD185627
LOCUS      Knockout animal.
DEFINITION
ACCESSION  BD185627
VERSION     BD185627.1 GI:31877827
KEYWORDS   JP 2002369689-A/6.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE   1 (bases 1 to 34)
AUTHORS     Ide,H., Yamamura,K. and Araki,K.
TITLE       Knockout animal
JOURNAL     Patent: JP 2002369689-A 6 24-DEC-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP,EU GENE LTD, PRESIDENT OF
              KUMAMOTO UNIVERSITY
COMMENT     OS Artificial Sequence
              PN JP 2002369689-A/6
              PD 24-DEC-2002
              PF 25-MAY-2001 JP 2001157568
              PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
              PC C12N15/09,A01K67/027,C12N5/10,C12N15/00,C12N5/00 CC
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              Location/Qualifiers
              FT source 1..34
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FEATURES
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1..34
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/db_xref="taxon:32630"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13
   |||||
Db 22 TATACGAACGGTA 34

RESULT 11
BD185627
LOCUS      Knockout animal.
DEFINITION
ACCESSION  BD185627
VERSION     BD185627.1 GI:31877827
KEYWORDS   JP 2002369689-A/6.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE   1 (bases 1 to 34)
AUTHORS     Ide,H., Yamamura,K. and Araki,K.
TITLE       Knockout animal
JOURNAL     Patent: JP 2002369689-A 6 24-DEC-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP,EU GENE LTD, PRESIDENT OF
              KUMAMOTO UNIVERSITY
COMMENT     OS Artificial Sequence
              PN JP 2002369689-A/6
              PD 24-DEC-2002
              PF 25-MAY-2001 JP 2001157568
              PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
              PC C12N15/09,A01K67/027,C12N5/10,C12N15/00,C12N5/00 CC
              Description of Artificial Sequence:synthetic DNA FH Key
              Location/Qualifiers
              FT source 1..34
              FT /organism='Artificial Sequence'.

FEATURES
source
1..34
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13
   |||||
Db 13 TATACGAACGGTA 1
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RESULT 13
AX114842
LOCUS AX114842 34 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2 from Patent WO0129208.
ACCESSION AX114842
VERSION AX114842.1 GI:14031784
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Kuehn,R., von Melchener,H. and Altschmied,J.
TITLE Conditional gene trapping construct for the disruption of genes
JOURNAL Patent: WO 0129208-A 2 26-APR-2001;
ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES
source
1..34
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="mutant loxp site - lox66"
ORIGIN
Query Match 100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATACGAACGGTA 13
|||
Db 22 TATACGAACGGTA 34

RESULT 14
AX114843/C
LOCUS AX114843 34 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 3 from Patent WO0129208.
ACCESSION AX114843
VERSION AX114843.1 GI:14031785
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Kuehn,R., von Melchener,H. and Altschmied,J.
TITLE Conditional gene trapping construct for the disruption of genes
JOURNAL Patent: WO 0129208-A 3 26-APR-2001;
ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES
source
1..34
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="mutant loxp site - lox71"
ORIGIN
Query Match 100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATACGAACGGTA 13
|||
Db 13 TATACGAACGGTA 1

RESULT 15
AX114844
LOCUS AX114844 34 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 4 from Patent WO0129208.
ACCESSION AX114844
VERSION AX114844.1 GI:14031786
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Kuehn,R., von Melchener,H. and Altschmied,J.
TITLE Conditional gene trapping construct for the disruption of genes
JOURNAL Patent: WO 0129208-A 4 26-APR-2001;
ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES
source
1..34
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="double mutant loxp site - lox66/71"
ORIGIN
Query Match 100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATACGAACGGTA 13
|||
Db 22 TATACGAACGGTA 34

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OM nucleic - nucleic search, using sw model

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(without alignments)
321.898 Million cell updates/sec

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Sequence: 1 tatacgaacggta 13

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Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	13	100.0	13	4	Aaf58481
C 3	13	100.0	13	8	Abz79455
C 4	13	100.0	13	8	Abz79456
C 5	13	100.0	33	8	Abv75983
C 6	13	100.0	33	8	Abv75984
C 7	13	100.0	34	4	Aaf58485
C 8	13	100.0	34	4	Aaf58485
C 9	13	100.0	34	5	Aad04917
C 10	13	100.0	34	5	Aad04918
C 11	13	100.0	34	5	Aad04918
C 12	13	100.0	34	5	Aad04916
C 13	13	100.0	34	6	Abn84175
C 14	13	100.0	34	6	Abn84176
C 15	13	100.0	34	6	Abn84176
C 16	13	100.0	34	6	Abn84176
C 17	13	100.0	34	8	Abv75996
C 18	13	100.0	34	8	Abv75996
C 19	13	100.0	34	8	Abz20929
C 20	13	100.0	34	8	Abz20924
C 21	13	100.0	34	8	Abz79444

22	13	100.0	34	8	Abz79445
23	13	100.0	34	8	Abz79449
C 24	13	100.0	34	8	Abz79449
C 25	13	100.0	34	9	Acc85309
26	13	100.0	34	9	Acc85308
27	13	100.0	34	10	Add13802
C 28	13	100.0	34	10	Add13801
C 29	13	100.0	34	10	Add13801
C 30	13	100.0	34	10	Add15151
C 31	13	100.0	34	10	Add15152
C 32	13	100.0	34	10	Add15152
33	13	100.0	34	10	Add15150
34	13	100.0	34	10	Abz75320
35	13	100.0	34	10	Abz75324
C 36	13	100.0	34	10	Abz75324
C 37	13	100.0	34	10	Abz75319
C 38	13	100.0	40	4	Aah44859
C 39	13	100.0	44	8	Abz20935
C 40	13	100.0	44	8	Abz20936
C 41	13	100.0	67	8	Abz20923
C 42	13	100.0	68	8	Abz20922
C 43	13	100.0	78	5	Aad04925
C 44	13	100.0	79	5	Aad04926
C 45	13	100.0	94	8	Abv75594
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ALIGNMENTS

RESULT 1
AAF58480/c
ID AAF58480 standard; DNA; 13 BP.
AC AAF58480;
XX
DT 24-APR-2001 (first entry)
DE Oligonucleotide: SEQ ID 1.
XX
KW Trap vector; loxp; gene therapy; gene trapping; ds.
XX
OS Unidentified.
XX
PN WO200105987-A1.
XX
PD 25-JAN-2001.
XX
PF 02-MAY-2000; 2000WO-JP002916.
XX
PR 14-JUL-1999; 99JP-00200997.
XX
PA (TRAN-) TRANSGENIC INC.
XX
PI Yamamura K, Araki K;
XX
DR WPI; 2001-159541/16.
XX
PT New trap vector, useful for gene trapping method for the efficient
production of gene-disrupted animals for investigating human diseases and
drug development, comprises a mutated loxp.
XX
PS Claim 3; Page 11; 55pp; Japanese.
XX
CC The present invention relates to a trap vector comprising a mutated loxp
in which a mutation is transferred into a part of a reversed repetitive
sequence in the loxp sequence. The vector is useful in the gene trapping
method for production of gene-disrupted animals in studying gene
functions, constructing model animals for investigating human diseases
and drug development, and gene therapy. The present sequence is an
oligonucleotide used in the present invention
XX
SQ Sequence 13 BP; 3 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

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Query Match      100.0%; Score 13; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
DB      13 TATACGAACGGTA 1

RESULT 2
AAF58481
ID AAF58481 standard; DNA; 13 BP.
XX
AC AAF58481;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide: SEQ ID 2.
XX
KW Trap vector; loxP; gene therapy; gene trapping; ds.
XX
OS Unidentified.
XX
PN WO200105987-A1.
XX
PD 25-JAN-2001.
XX
PF 02-MAY-2000; 2000WO-JP002916.
XX
PR 14-JUL-1999; 99JP-00200997.
XX
PA (TRAN-) TRANSGENIC INC.
XX
PI Yamamura K, Araki K;
XX
DR WPI; 2001-159541/16.
XX
PT New trap vector, useful for gene trapping method for the efficient
PT production of gene-disrupted animals for investigating human diseases and
PT drug development, comprises a mutated loxP.
XX
PS Claim 6; Page 12; 55pp; Japanese.
XX
CC The present invention relates to a trap vector comprising a mutated loxP
CC in which a mutation is transferred into a part of a reversed repetitive
CC sequence in the loxP sequence. The vector is useful in the gene trapping
CC method for production of gene-disrupted animals in studying gene
CC functions, constructing model animals for investigating human diseases
CC and drug development, and gene therapy. The present sequence is an
CC oligonucleotide used in the present invention
XX
SQ Sequence 13 BP; 5 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match      100.0%; Score 13; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
DB      13 TATACGAACGGTA 1

RESULT 3
ABZ79455/c
ID ABZ79455 standard; DNA; 13 BP.
XX
AC ABZ79455;
XX
DT 23-MAY-2003 (first entry)
XX
DE DNA sequence related to the chimera mouse of the invention #1.
XX
KW LoxP; knockout mouse; vascularisation; embryonic stem cell;

Query Match      100.0%; Score 13; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
DB      13 TATACGAACGGTA 13

RESULT 4
ABZ79456
ID ABZ79456 standard; DNA; 13 BP.
XX
AC ABZ79456;
XX
DT 23-MAY-2003 (first entry)
XX
DE DNA sequence related to the chimera mouse of the invention #2.
XX
KW LoxP; knockout mouse; vascularisation; embryonic stem cell;
KW drug development; locus of crossing over; ds.
XX
OS Unidentified.
XX
PN JP2002369689-A.
XX
PD 24-DEC-2002.
XX
PF 25-MAY-2001; 2001JP-00157568.
XX
PR 25-MAY-2001; 2001JP-00157568.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (IDEH/) IDE H.
PA (YANA/) YAMAMURA K.
PA (ARAK/) ARAKI Y.
XX
DR WPI; 2003-125824/12.

KW drug development; locus of crossing over; ds.
XX
OS Unidentified.
XX
PN JP2002369689-A.
XX
PD 24-DEC-2002.
XX
PF 25-MAY-2001; 2001JP-00157568.
XX
PR 25-MAY-2001; 2001JP-00157568.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (IDEH/) IDE H.
PA (YANA/) YAMAMURA K.
PA (ARAK/) ARAKI Y.
XX
DR WPI; 2003-125824/12.

Query Match      100.0%; Score 13; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
DB      13 TATACGAACGGTA 1

RESULT 5
ABZ79457
ID ABZ79457 standard; DNA; 13 BP.
XX
AC ABZ79457;
XX
DT 23-MAY-2003 (first entry)
XX
DE DNA sequence related to the chimera mouse of the invention #3.
XX
KW LoxP; knockout mouse; vascularisation; embryonic stem cell;
KW drug development; locus of crossing over; ds.
XX
OS Unidentified.
XX
PN JP2002369689-A.
XX
PD 24-DEC-2002.
XX
PF 25-MAY-2001; 2001JP-00157568.
XX
PR 25-MAY-2001; 2001JP-00157568.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (IDEH/) IDE H.
PA (YANA/) YAMAMURA K.
PA (ARAK/) ARAKI Y.
XX
DR WPI; 2003-125824/12.
```

XX Knockout mouse or embryonic stem cells with introduced trap vectors
 PT containing a loxp sequence or a variant loxp sequence with disrupted gene
 PT of sequence No. 7 of 1405 bases.

XX PS Disclosure; Page 6; 21pp; Japanese.

XX CC The invention relates to a knockout mouse or embryonic stem cells with
 CC introduced trap vectors containing a loxp sequence. The knockout animals
 CC of the invention may be used in the analysis of genomic functions, and
 CC particularly for investigating the processes of vascularisation and the
 CC development of drugs participating in such processes. The current
 CC sequence represents a DNA sequence related to the chimera mouse of the
 CC invention

XX SQ Sequence 13 BP; 5 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 13; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGACGGTA 13

DB 1 TATACGACGGTA 13

RESULT 5

ABV75983/C
 ID ABV75983 standard; DNA; 33 BP.

AC ABV75983;

DT 11-FEB-2003 (first entry)

DE Modified left element loxp site.

XX LoxP; phage P1; recombination; minicircle; gene therapy; mitochondria;
 KW mutant; ss.

XX Bacteriophage p1.

OS Synthetic.

XX WO200283889-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-GB001668.

XX 10-APR-2001; 2001GB-00008968.

PR 05-OCT-2001; 2001US-0327029P.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

PI Bigger BW, Tolmachov O, Coutelle C;

XX WPI; 2003-075546/07.

XX CC New cell capable of expressing an endonuclease, useful for producing a
 PT minicircle for mitochondrial gene therapy, comprises a parent plasmid
 PT capable of recombination to form a minicircle and a miniplasmid.

XX PS Disclosure; Page 4; 70pp; English.

XX CC The present sequence is that of a left element (LE) loxp site in which
 CC the 5 nucleotides at the 5' end of loxp have been modified. The LE loxp
 CC site is used in the method of the invention for the production of a
 CC minicircle. In this method, a parent plasmid is provided which has a
 CC nucleic acid sequence flanked by recombination sites. The plasmid is
 CC exposed to an enzyme which causes recombination at the recombination
 CC sites, forming (i) a minicircle comprising the nucleic acid sequence and
 CC (ii) a miniplasmid comprising the remainder of the parent plasmid. One
 CC recombination site is modified at the 5' end such that its reaction with
 CC the enzyme is less efficient than the wild-type site, and the other

CC recombination site is modified at the 3' end such that its reaction with
 CC the enzyme is less efficient than the wild-type site, both modified sites
 CC being located in the minicircle after recombination. This favours the
 CC formation of the minicircle. In a preferred embodiment, the enzyme is Cre
 CC recombinase and the recombination sites are loxp sites. The method is
 CC preferably carried out in a bacterium, especially Escherichia coli. The
 CC minicircle can be used for mitochondrial gene therapy

XX SQ Sequence 33 BP; 10 A; 6 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 100.0%; Score 13; DB 8; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGACGGTA 13

DB 13 TATACGACGGTA 1

RESULT 6

ABV75984

ID ABV75984 standard; DNA; 33 BP.

AC ABV75984;

DT 11-FEB-2003 (first entry)

DE Modified right element loxp site.

XX LoxP; phage P1; recombination; minicircle; gene therapy; mitochondria;
 KW mutant; ss.

XX Bacteriophage p1.

OS Synthetic.

XX WO200283889-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-GB001668.

XX 10-APR-2001; 2001GB-00008968.

PR 05-OCT-2001; 2001US-0327029P.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

PI Bigger BW, Tolmachov O, Coutelle C;

XX WPI; 2003-075546/07.

XX CC New cell capable of expressing an endonuclease, useful for producing a
 PT minicircle for mitochondrial gene therapy, comprises a parent plasmid
 PT capable of recombination to form a minicircle and a miniplasmid.

XX PS Disclosure; Page 4; 70pp; English.

XX CC The present sequence is that of a right element (RE) loxp site in which
 CC the 5 nucleotides at the 3' end of loxp have been modified. The RE loxp
 CC site is used in the method of the invention for the production of a
 CC minicircle. In this method, a parent plasmid is provided which has a
 CC nucleic acid sequence flanked by recombination sites. The plasmid is
 CC exposed to an enzyme which causes recombination at the recombination
 CC sites, forming (i) a minicircle comprising the nucleic acid sequence and
 CC (ii) a miniplasmid comprising the remainder of the parent plasmid. One
 CC recombination site is modified at the 5' end such that its reaction with
 CC the enzyme is less efficient than the wild-type site, and the other
 CC recombination site is modified at the 3' end such that its reaction with
 CC the enzyme is less efficient than the wild-type site, both modified sites
 CC being located in the minicircle after recombination. This favours the
 CC formation of the minicircle. In a preferred embodiment, the enzyme is Cre
 CC recombinase and the recombination sites are loxp sites. The method is
 CC preferably carried out in a bacterium, especially Escherichia coli. The
 CC minicircle can be used for mitochondrial gene therapy

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XX SQ Sequence 33 BP; 12 A; 6 C; 5 G; 10 T; 0 U; 0 Other;
Query Match 100.0%; Score 13; DB 8; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13
DB 21 TATACGAACGGTA 33

RESULT 7
AAF58485
ID AAF58485 standard; DNA; 34 BP.
AC AAF58485;
XX 24-APR-2001 (first entry)
XX Oligonucleotide: SEQ ID 6.
XX Trap vector; loxP; gene therapy; gene trapping; ds.
XX Unidentified.
XX WO200105987-A1.
XX 25-JAN-2001.
XX 02-MAY-2000; 2000WO-JP002916.
XX 14-JUL-1999; 99JP-00200997.
XX (TRAN-) TRANSGENIC INC.
XX Yamamura K, Araki K;
XX WPI; 2001-159541/16.
XX New trap vector, useful for gene trapping method for the efficient
XX production of gene-disrupted animals for investigating human diseases and
XX drug development, comprises a mutated loxP.
XX Disclosure; Fig 4; 55pp; Japanese.
XX The present invention relates to a trap vector comprising a mutated loxP
XX in which a mutation is transferred into a part of a reversed repetitive
XX sequence in the loxP sequence. The vector is useful in the gene trapping
XX method for production of gene-disrupted animals in studying gene
XX functions, constructing model animals for investigating human diseases
XX and drug development, and gene therapy. The present sequence is an
XX oligonucleotide used in the present invention
XX SQ Sequence 34 BP; 11 A; 7 C; 6 G; 10 T; 0 U; 0 Other;
Query Match 100.0%; Score 13; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13
DB 13 TATACGAACGGTA 1

RESULT 9
AAD04917/c
ID AAD04917 standard; DNA; 34 BP.
XX AAD04917;
XX 17-JUL-2001 (first entry)
XX Recombinase recognition sequence (RRS), loxP site mutant (lox71) DNA.
XX Gene trapping construct; conditional mutation; unidirectional inversion;
XX recombinase recognition sequence; RRS; disruption cassette;
XX selection cassette; transgenic organism; loxP site; mutant; ds.
XX Enterobacteria phage P1.
XX Synthetic.
XX WO200129208-A1.
XX 26-APR-2001.
XX 16-OCT-2000; 2000WO-EP010162.
XX 16-OCT-1999; 99EP-00120592.
XX 27-OCT-1999; 99US-0162016P.
XX (ARTE-) ARTEMIS PHARM GMBH.
XX (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
```


XX The present invention relates to a conditional gene trapping construct
 CC capable of causing conditional mutations in genes. The gene trapping
 CC construct comprises two functional DNA segments, each being flanked by
 CC two recombinase recognition sequences (RRSs) specific to site specific
 CC recombinase which is capable of unidirectional inversion of double
 CC standard DNA segment. One of the DNA segment (disruption cassette) is
 CC inserted in antisense orientation relative to the transcriptional
 CC orientation of the gene to be trapped. The other DNA segment (selection
 CC cassette) is inserted in sense direction relative to the transcriptional
 CC orientation of the gene to be trapped. The cell comprising the gene
 CC trapping construct is useful for the identification and/or isolation of
 CC genes. The transgenic organism comprising the gene trapping construct is
 CC useful to study gene function at various developmental stages. The gene
 CC trapping construct is useful for mutationally inactivating all cellular
 CC genes. The present DNA sequence encodes recombinase recognition sequence,
 CC loxP site double mutant (lox71/lox66), which flanks the functional DNA
 CC segments of gene trapping construct
 XX Sequence 34 BP; 11 A; 7 C; 6 G; 10 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 13; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TATACGAACGGTA 13
 DB 13 TATACGAACGGTA 1
 RESULT 12
 AAD04916
 ID AAD04916 standard; DNA; 34 BP.
 AC
 XX
 XX AAD04916;
 DT 17-JUL-2001 (first entry)
 DE Recombinase recognition sequence (RRS), loxP site mutant (lox66) DNA.
 XX
 XX Gene trapping construct; conditional mutation; unidirectional inversion;
 KW recombinase recognition sequence; RRS; disruption cassette;
 KW selection cassette; transgenic organism; loxP site; mutant; ds.
 XX
 OS Enterobacteria phage P1.
 OS Synthetic.
 XX
 XX WO200129208-A1.
 XX
 XX 26-APR-2001.
 XX
 XX 16-OCT-2000; 2000WO-EP010162.
 PF
 XX 16-OCT-1999; 99EP-00120592.
 PR 27-OCT-1999; 99US-0162016P.
 XX
 XX (ARTE-) ARTEMIS PHARM GMBH.
 PA (FRAN-) FRANKEN BIOTECHNOLOGIE AG.
 XX
 XX Kuehn R, Von Melchener H, Altschmied J;
 PI WPI; 2001-308486/32.
 DR
 XX
 XX New gene trapping construct capable of causing conditional mutations in
 PT genes, comprises functional DNA segment inserted in sense or antisense
 PT direction relative to gene to be trapped.
 XX
 XX Claim 4; Page 49; 78pp; English.
 PS
 XX The present invention relates to a conditional gene trapping construct
 CC capable of causing conditional mutations in genes. The gene trapping
 CC construct comprises two functional DNA segments, each being flanked by
 CC two recombinase recognition sequences (RRSs) specific to site specific

CC recombinase which is capable of unidirectional inversion of double
 CC standard DNA segment. One of the DNA segment (disruption cassette) is
 CC inserted in antisense orientation relative to the transcriptional
 CC orientation of the gene to be trapped. The other DNA segment (selection
 CC cassette) is inserted in sense direction relative to the transcriptional
 CC orientation of the gene to be trapped. The cell comprising the gene
 CC trapping construct is useful for the identification and/or isolation of
 CC genes. The transgenic organism comprising the gene trapping construct is
 CC useful to study gene function at various developmental stages. The gene
 CC trapping construct is useful for mutationally inactivating all cellular
 CC genes. The present DNA sequence encodes recombinase recognition sequence,
 CC loxP site mutant (lox66), which flanks the functional DNA segments of
 CC gene trapping construct
 XX Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 13; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TATACGAACGGTA 13
 DB 22 TATACGAACGGTA 34
 RESULT 13
 ABN84175
 ID ABN84175 standard; DNA; 34 BP.
 AC
 XX
 XX ABN84175;
 DT 23-SEP-2002 (first entry)
 DE LoxP left element mutant.
 XX
 XX Gene inactivation; mutagenesis; vector; knockout animal;
 KW transgenic animal; gene trapping; loxP; mutant; ss.
 XX
 OS Enterobacteria phage P1.
 OS Synthetic.
 XX
 XX WO200240685-A2.
 PN
 XX 23-MAY-2002.
 PD
 XX 16-NOV-2001; 2001WO-US043916.
 PF
 XX 16-NOV-2000; 2000US-0249200P.
 PR (CORR) CORNELL RES FOUND INC.
 XX
 XX Xin H, Kotlikoff M;
 PI
 XX WPI; 2002-537342/57.
 DR
 XX Novel genetically engineered vector comprising gene trap cassette, and
 PT mutational element cassette that is transcriptionally silent, but which
 PT is activated by recombinase expression to disrupt expression of trapped
 PT gene.
 XX
 XX Example 2; Page 35; 58pp; English.
 PS
 XX The present invention provides recombinant vectors and methods of using
 CC the vectors in a high-throughput genetic system to rapidly generate
 CC conditional and/or conventional knockout mutants, e.g. in mice, useful
 CC for identifying and defining mammalian gene function in vivo. The methods
 CC combine gene trapping, gene targeting, and site-specific recombination
 CC techniques. The vectors comprise a transcriptionally silent mutational
 CC element that is inserted within a gene in a target cell in a manner that
 CC retains gene function, and which can be manipulated to inactivate the
 CC gene when desired. The mutational element may be flanked by mutant loxP
 CC sites in a manner that produces a directional bias toward inversion of
 CC the mutational sequence upon exposure to cre recombinase. Once inverted,

CC the mutational element is spliced into the trapped gene resulting in
CC expression of a reporter gene and premature termination of the endogenous
CC mRNA. Site-directed DNA integration is achieved using a pair of mutant
CC loxP sites, a right element (RE) mutant (see ABN84176) and a left element
CC (LE) mutant (present sequence). The mutant loxP system produces a
CC reaction biased toward an irreversible gene inversion. The method of the
CC invention facilitates investigation of the function of individual genes
CC by a rapid extension of the conditional knockout approach

XX Sequence 34 BP; 12 A; 5 C; 6 G; 11 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGACGGTA 13
DB 22 TATACGACGGTA 34

RESULT 14
ABN84176
ID ABN84176 standard; DNA; 34 BP.

XX AC ABN84176;

XX DT 23-SEP-2002 (first entry)

XX DE LoxP right element mutant.

XX Gene inactivation; mutagenesis; vector; knockout animal;
KW transgenic animal; gene trapping; loxP; mutant; ss.

XX Enterobacteria phage P1.

OS Synthetic.

XX WO200240685-A2.

XX 23-MAY-2002.

XX PF 16-NOV-2001; 2001WO-US043916.

XX PR 16-NOV-2000; 2000US-0249200P.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Xin H, Kotlikoff M;

XX WPI; 2002-537342/57.

XX Novel genetically engineered vector comprising gene trap cassette, and
PT mutational element cassette that is transcriptionally silent, but which
PT is activated by recombinase expression to disrupt expression of trapped
PT gene.

XX Example 2; Page 35; 58pp; English.

XX The present invention provides recombinant vectors and methods of using
CC the vectors in a high-throughput genetic system to rapidly generate
CC conditional and/or conventional knockout mutants, e.g. in mice, useful
CC for identifying and defining mammalian gene function in vivo. The methods
CC combine gene trapping, gene targeting, and site-specific recombinational
CC techniques. The vectors comprise a transcriptionally silent mutational
CC element that is inserted within a gene in a target cell in a manner that
CC retains gene function, and which can be manipulated to inactivate the
CC gene when desired. The mutational element may be flanked by mutant LoxP
CC sites in a manner that produces a directional bias toward inversion of
CC the mutational sequence upon exposure to cre recombinase. Once inverted,
CC the mutational element is spliced into the trapped gene resulting in
CC expression of a reporter gene and premature termination of the endogenous
CC mRNA. Site-directed DNA integration is achieved using a pair of mutant
CC loxP sites, a right element (RE) mutant (present sequence) and a left
CC element (LE) mutant (see ABN84175). The mutant loxP system produces a

CC reaction biased toward an irreversible gene inversion. The method of the
CC invention facilitates investigation of the function of individual genes
CC by a rapid extension of the conditional knockout approach

XX Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGACGGTA 13
DB 22 TATACGACGGTA 34

RESULT 15
ABA03776
ID ABA03776 standard; DNA; 34 BP.

XX AC ABA03776;

XX DT 19-FEB-2002 (first entry)

XX DE Synthetic lox66 sequence.

XX lox66; gene therapy; gene targeting; gene trapping;

KW antisense RNA production; ds.

XX OS Synthetic.

XX WO200185973-A1.

XX PD 15-NOV-2001.

XX PF 29-AUG-2000; 2000WO-JP005824.

XX PR 11-MAY-2000; 2000JP-00138938.

XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX PI Taniguchi M, Karasawa M;

XX WPI; 2002-055602/07.

XX Antisense type gene trap vector, useful for gene therapy of diseases and
PT production of animal models for disease study, disrupts transcription of
PT specific gene.

XX Claim 19; Page 43; 48pp; Japanese.

XX The invention relates to a method for producing cells in which the
CC expression of a gene is disrupted. The cells are transformed with a gene
CC trap vector to give a trap clone having the vector inserted at a specific
CC mutation site of the target gene. The trap clone is then transformed with
CC a vector that inserts a promoter in the antisense direction of the gene,
CC enforcing transcription of antisense RNA. The method is useful for the
CC production of animal models for studying human diseases. It is also
CC useful as gene therapy for the treatment and prevention of diseases. The
CC present sequence is a lox66 sequence claimed in the specification

XX Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 13; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGACGGTA 13
DB 22 TATACGACGGTA 34

Search completed: December 24, 2004, 08:41:54
Job time : 213 secs

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 08:14:39 ; Search time 49 Seconds
(without alignments)
188.577 Million cell updates/sec

Title: US-10-030-658B-2
Perfect score: 13
Sequence: 1 tatacgacggta 13

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*

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- 2: /cgn2_6/ptodata1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata1/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	92.3	606	4	US-09-270-767-7235, Ap
C 2	12	92.3	606	4	US-09-270-767-22517, A
C 3	12	92.3	630	4	US-09-270-767-10568, A
C 4	12	92.3	960	4	US-09-328-352-580, App
C 5	12	92.3	2142	4	US-09-614-221A-331, App
C 6	11.4	87.7	249	4	US-09-107-532A-1707, Ap
C 7	11.4	87.7	261	1	US-08-307-499-39, Appl
C 8	11.4	87.7	261	3	US-09-299-268-39, Appl
C 9	11.4	87.7	285	1	US-07-675-772-6, Appl
C 10	11.4	87.7	293	4	US-09-313-294A-1338, Ap
C 11	11.4	87.7	354	4	US-09-614-221A-215, App
C 12	11.4	87.7	381	5	PCT-US96-04648-5, Appl
C 13	11.4	87.7	437	4	US-09-270-767-7147, Ap
C 14	11.4	87.7	437	4	US-09-270-767-22429, A
C 15	11.4	87.7	498	4	US-09-489-039A-6859, Ap
C 16	11.4	87.7	702	4	US-09-270-767-9448, Ap
C 17	11.4	87.7	702	4	US-09-270-767-24730, A
C 18	11.4	87.7	705	1	US-08-178-242-7, Appl
C 19	11.4	87.7	705	2	US-08-955-091-7, Appl
C 20	11.4	87.7	705	3	US-09-225-510-7, Appl
C 21	11.4	87.7	715	4	US-09-270-767-10243, A
C 22	11.4	87.7	741	3	US-08-998-416-953, Appl
C 23	11.4	87.7	751	4	US-09-687-698-1, Appl
C 24	11.4	87.7	751	4	US-09-705-621-17, Appl
C 25	11.4	87.7	758	2	US-08-720-258-1, Appl
C 26	11.4	87.7	801	4	US-09-248-796A-3243, Ap
C 27	11.4	87.7	831	4	US-09-489-039A-2499, Ap

ALIGNMENTS

RESULT 1

US-09-270-767-7235/c
; Sequence 7235, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7235
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-7235

Query Match 92.3%; Score 12; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ATACGACGGTA 13
Db 583 ATACGACGGTA 572

RESULT 2

US-09-270-767-22517/c
; Sequence 22517, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22517
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-22517

Query Match 92.3%; Score 12; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ATACGACGGTA 13

Db 583 ATACGAACGGTA 572
|||||

RESULT 3

US-09-270-767-10568/c
; Sequence 10568, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10568
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10568

Query Match 92.3%; Score 12; DB 4; Length 630;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATACGAACGGTA 13
|||||

Db 421 ATACGAACGGTA 410
|||||

RESULT 4

US-09-328-352-580
; Sequence 580, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: GTC99-03PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 580
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-580

Query Match 92.3%; Score 12; DB 4; Length 960;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATACGAACGGTA 13
|||||

Db 173 ATACGAACGGTA 184
|||||

RESULT 5

US-09-614-221A-331/c
; Sequence 331, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasubrajini
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; WITH STEROL SYNTHESIS AND METABOLISM
; FILE REFERENCE: 15516.075
; CURRENT APPLICATION NUMBER: US/09/614,221A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/142,981
; PRIOR FILING DATE: 1999-07-12

Query Match 87.7%; Score 11.4; DB 4; Length 249;
Best Local Similarity 92.3%; Pred. No. 3.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

; NUMBER OF SEQ ID NOS: 626

; SEQ ID NO 331

; LENGTH: 2142

; TYPE: DNA

; ORGANISM: Saccharomyces cerevisiae

US-09-614-221A-331

Query Match 92.3%; Score 12; DB 4; Length 2142;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATACGAACGGTA 13
|||||

Db 1532 ATACGAACGGTA 1521
|||||

RESULT 6

US-09-107-532A-1707
; Sequence 1707, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1707:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...249
; SEQUENCE DESCRIPTION: SEQ ID NO: 1707:

US-09-107-532A-1707

QY 1 TATACGAACGGTA 13
|||||||
Db 163 TATACGAATGGTA 175

RESULT 7
US-08-307-499-39
; Sequence 39, Application US/08307499
; Patent No. 5651972
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Gibbs, E.P.J.
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
; TITLE OF INVENTION: Live Vaccine Vector
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,499
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,241
; FILING DATE: 1-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,630
; FILING DATE: 29-JUN-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/342,212
; FILING DATE: 21-APR-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-307-499-39

Query Match 87.7%; Score 11.4; DB 1; Length 261;
Best Local Similarity 92.3%; Pred. No. 3.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13
|||||||
Db 223 TATACGAACGATA 235

RESULT 8
US-09-299-268-39
; Sequence 39, Application US/09299268
; Patent No. 6217882
; GENERAL INFORMATION:

; APPLICANT: Moyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Gibbs, E.P.J.
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
; TITLE OF INVENTION: Live Vaccine Vector
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/901,127
; FILING DATE:
; APPLICATION NUMBER: US 07/908,241
; FILING DATE: 1-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,630
; FILING DATE: 29-JUN-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/342,212
; FILING DATE: 21-APR-1992
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-09-299-268-39

Query Match 87.7%; Score 11.4; DB 3; Length 261;
Best Local Similarity 92.3%; Pred. No. 3.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13
|||||||
Db 223 TATACGAACGATA 235

RESULT 9
US-07-675-772-6
; Sequence 6, Application US/07675772
; Patent No. 5262399
; GENERAL INFORMATION:
; APPLICANT: Hickie, Leslie A.
; APPLICANT: Sick, August J.
; APPLICANT: Schwab, George E.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Payne, Jewel M.
; TITLE OF INVENTION: No. 5262399el Compositions and Methods for the Control of
; TITLE OF INVENTION: Flukes
; NUMBER OF SEQUENCES: 6

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: ROMAN SALIWANCHIK
;; STREET: 2421 N.W. 41st Street, Suite A-1
;; CITY: Gainesville
;; STATE: FL
;; COUNTRY: USA
;; ZIP: 32606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/675,772
;; FILING DATE: 19910327
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SALIWANCHIK, ROMAN
;; REGISTRATION NUMBER: 21,023
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 904-375-8100
;; TELEFAX: 904-372-5800
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 285 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;;
US-07-675-772-6

Query Match 87.7%; Score 11.4; DB 1; Length 285;
Best Local Similarity 92.3%; Pred. No. 3.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13
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Db 217 TATACGAATGGTA 229

RESULT 10
US-09-313-294A-1338
;; Sequence 1338, Application US/09313294A
;; Patent No. 6476212
;; GENERAL INFORMATION:
;; APPLICANT: Lalgudi, Raghunath V.
;; APPLICANT: Ito, Laura Y.
;; APPLICANT: Sherman, Bradley K.
;; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
;; FILE REFERENCE: PL-0017 US
;; CURRENT APPLICATION NUMBER: US/09/313,294A
;; CURRENT FILING DATE: 1999-05-14
;; NUMBER OF SEQ ID NOS: 7600
;; SOFTWARE: PERL Program
;; SEQ ID NO 1338
;; LENGTH: 293
;; TYPE: DNA
;; ORGANISM: Zea mays
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte ID No. 6476212 700550765H1
US-09-313-294A-1338

Query Match 87.7%; Score 11.4; DB 4; Length 293;
Best Local Similarity 92.3%; Pred. No. 3.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13
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Db 280 TATCGAACGGTA 292

RESULT 11
US-09-614-221A-215

;; Sequence 215, Application US/09614221A
;; Patent No. 6723837
;; GENERAL INFORMATION:
;; APPLICANT: Karunanandaa, Balasulojini
;; APPLICANT: Yu, Jaehyuk
;; APPLICANT: Kishore, Ganesh M.
;; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
;; WITH STEROL SYNTHESIS AND METABOLISM
;; FILE REFERENCE: 16516.075
;; CURRENT APPLICATION NUMBER: US/09/614,221A
;; CURRENT FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/142,981
;; PRIOR FILING DATE: 1999-07-12
;; NUMBER OF SEQ ID NOS: 626
;; SEQ ID NO 215
;; LENGTH: 354
;; TYPE: DNA
;; ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-215

Query Match 87.7%; Score 11.4; DB 4; Length 354;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13
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Db 125 TATACGAACGTA 137

RESULT 12
PCT-US96-04648-5/c
;; Sequence 5, Application PC/TUS9604648
;; GENERAL INFORMATION:
;; APPLICANT: Cell Genesys, Inc.
;; TITLE OF INVENTION: Transplantation of Genetically Modified Cells Having Low Leve
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
;; STREET: 4 Embarcadero Center, Suite 3400
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 941114187
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy Disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PCDOS/MSDOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/04648
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sherwood, Pamela J
;; REGISTRATION NUMBER: 36,677
;; REFERENCE/DOCKET NUMBER: Cell 23-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415494-8700
;; TELEFAX: 415494-8771
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 381 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
PCT-US96-04648-5

Query Match 87.7%; Score 11.4; DB 5; Length 381;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13

Db 122 TCTACGACGGTA 110
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RESULT 13

US-09-270-767-7147/c
; Sequence 7147, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7147
; LENGTH: 437
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-7147

Query Match 87.7%; Score 11.4; DB 4; Length 437;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TATACGACGGTA 13
| ||||| |||||
Db 28 TATACGACTGTA 16

RESULT 14

US-09-270-767-22429/c
; Sequence 22429, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22429
; LENGTH: 437
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-22429

Query Match 87.7%; Score 11.4; DB 4; Length 437;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TATACGACGGTA 13
| ||||| |||||
Db 28 TATACGACTGTA 16

RESULT 15

US-09-489-039A-6859
; Sequence 6859, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6859

; LENGTH: 498
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6859

Query Match 87.7%; Score 11.4; DB 4; Length 498;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TATACGACGGTA 13
| ||||| |||||
Db 118 TATCCGAACGGTA 130

Search completed: December 24, 2004, 10:12:53
Job time : 49 secs

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 09:10:55 ; Search time 221.5 Seconds
(without alignments)
326.801 Million cell updates/sec

Title: US-10-030-658B-2

Perfect score: 13

Sequence: 1 tatacgaacggta 13

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4105333 seqs, 2784095677 residues

Total number of hits satisfying chosen parameters: 8210666

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13	100.0	33	14	US-10-118-231-1
C 2	13	100.0	33	14	US-10-118-231-2
C 3	13	100.0	34	10	US-09-957-660-2
C 4	13	100.0	34	10	US-09-957-660-3
C 5	13	100.0	34	10	US-09-957-660-4
C 6	13	100.0	34	10	US-09-957-660-4
C 7	13	100.0	34	14	US-10-118-231-18
C 8	13	100.0	34	14	US-10-214-722-1
C 9	13	100.0	34	14	US-10-214-722-6
C 10	13	100.0	34	14	US-10-214-722-8
C 11	13	100.0	34	16	US-10-416-995-9
C 12	13	100.0	34	16	US-10-416-995-10

13	13	100.0	34	17	US-10-739-769-2	Sequence 2, Appli
C 14	13	100.0	34	17	US-10-739-769-3	Sequence 3, Appli
C 15	13	100.0	34	17	US-10-739-769-4	Sequence 4, Appli
C 16	13	100.0	34	17	US-10-739-769-4	Sequence 4, Appli
C 17	13	100.0	34	17	US-10-739-769-5	Sequence 5, Appli
C 18	13	100.0	34	17	US-10-739-769-6	Sequence 6, Appli
C 19	13	100.0	34	18	US-10-448-395-2	Sequence 8, Appli
C 20	13	100.0	34	18	US-10-448-395-8	Sequence 13, Appli
C 21	13	100.0	34	18	US-10-448-395-13	Sequence 13, Appli
C 22	13	100.0	34	18	US-10-448-395-14	Sequence 14, Appli
C 23	13	100.0	40	10	US-09-899-615-4	Sequence 4, Appli
C 24	13	100.0	40	18	US-10-448-395-15	Sequence 15, Appli
C 25	13	100.0	40	18	US-10-448-395-16	Sequence 16, Appli
C 26	13	100.0	40	18	US-10-448-395-17	Sequence 17, Appli
C 27	13	100.0	40	18	US-10-448-395-18	Sequence 18, Appli
C 28	13	100.0	44	14	US-10-214-722-14	Sequence 14, Appli
C 29	13	100.0	44	14	US-10-214-722-15	Sequence 15, Appli
C 30	13	100.0	67	14	US-10-214-722-12	Sequence 12, Appli
C 31	13	100.0	68	14	US-10-214-722-11	Sequence 11, Appli
C 32	13	100.0	94	14	US-10-118-231-10	Sequence 10, Appli
C 33	13	100.0	94	14	US-10-118-231-10	Sequence 10, Appli
C 34	13	100.0	94	14	US-10-118-231-16	Sequence 16, Appli
C 35	13	100.0	94	14	US-10-118-231-16	Sequence 16, Appli
C 36	13	100.0	485	16	US-10-424-599-20024	Sequence 20024, A
C 37	13	100.0	489	18	US-10-425-115-178519	Sequence 178519,
C 38	13	100.0	507	16	US-10-425-114-2962	Sequence 2962, Ap
C 39	13	100.0	951	9	US-09-727-855B-3	Sequence 3, Appli
C 40	13	100.0	1512	9	US-09-938-842A-801	Sequence 801, App
C 41	13	100.0	1512	11	US-09-938-842A-801	Sequence 801, App
C 42	13	100.0	2133	18	US-10-448-395-1	Sequence 1, Appli
C 43	12	92.3	242	16	US-10-424-599-139159	Sequence 139159,
C 44	12	92.3	287	18	US-10-425-115-110479	Sequence 110479,
C 45	12	92.3	491	17	US-10-437-963-17515	Sequence 17515, A

ALIGNMENTS

RESULT 1
US-10-118-231-1/c
; Sequence 1, Application US/10118231
; Publication NO. US20030005478A1
; GENERAL INFORMATION:
; APPLICANT: Bigger, Brian W
; APPLICANT: Tolmachov, Oleg
; APPLICANT: Coutelle, Charles
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 102286.141US
; CURRENT APPLICATION NUMBER: US/10/118,231
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/327,029
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: GB 0108968.9
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: left element
; OTHER INFORMATION: (LB) loxp site (also known as lox71)
US-10-118-231-1

Query Match 100.0%; Score 13; DB 14; Length 33;
Best Local Similarity 100.0%; Pred. NO. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATACGACGGTA 13
DB 13 TATACGACGGTA 1

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RESULT 2
US-10-118-231-2
; Sequence 2, Application US/10118231
; Publication No. US20030005478A1
; GENERAL INFORMATION:
; APPLICANT: Bigger, Brian W
; APPLICANT: Tolmachev, Oleg
; APPLICANT: Coutelle, Charles
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 102286.141US
; CURRENT FILING DATE: 2001-04-10
; CURRENT APPLICATION NUMBER: US/10/118,231
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/327,029
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: GB 0108968.9
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: right element
; OTHER INFORMATION: (RE) loxp site (also known as lox66)
US-10-118-231-2

Query Match      100.0%; Score 13; DB 14; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
DB      21 TATACGAACGGTA 33

RESULT 3
US-09-957-660-2
; Sequence 2, Application US/09957660
; Publication No. US20030100077A1
; GENERAL INFORMATION:
; APPLICANT: KORTE, JOHN A.
; TITLE OF INVENTION: IN VITRO METHOD TO CREATE CIRCULAR MOLECULES FOR USE IN
; FILE REFERENCE: DEKM:176US
; CURRENT APPLICATION NUMBER: US/09/957,660
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-957-660-2

Query Match      100.0%; Score 13; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
DB      22 TATACGAACGGTA 34

RESULT 4
US-09-957-660-3/c
; Sequence 3, Application US/09957660
; Publication No. US20030100077A1
; GENERAL INFORMATION:
; APPLICANT: KORTE, JOHN A.
; TITLE OF INVENTION: IN VITRO METHOD TO CREATE CIRCULAR MOLECULES FOR USE IN
; FILE REFERENCE: DEKM:176US
; CURRENT APPLICATION NUMBER: US/09/957,660
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 16
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; GENERAL INFORMATION:
; APPLICANT: KORTE, JOHN A.
; APPLICANT: LOWE, BRENDA A.
; TITLE OF INVENTION: IN VITRO METHOD TO CREATE CIRCULAR MOLECULES FOR USE IN
; FILE REFERENCE: DEKM:176US
; CURRENT APPLICATION NUMBER: US/09/957,660
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-957-660-3

Query Match      100.0%; Score 13; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
DB      13 TATACGAACGGTA 1

RESULT 5
US-09-957-660-4
; Sequence 4, Application US/09957660
; Publication No. US20030100077A1
; GENERAL INFORMATION:
; APPLICANT: KORTE, JOHN A.
; TITLE OF INVENTION: IN VITRO METHOD TO CREATE CIRCULAR MOLECULES FOR USE IN
; FILE REFERENCE: DEKM:176US
; CURRENT APPLICATION NUMBER: US/09/957,660
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-957-660-4

Query Match      100.0%; Score 13; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
DB      22 TATACGAACGGTA 34

RESULT 6
US-09-957-660-4/c
; Sequence 4, Application US/09957660
; Publication No. US20030100077A1
; GENERAL INFORMATION:
; APPLICANT: KORTE, JOHN A.
; TITLE OF INVENTION: IN VITRO METHOD TO CREATE CIRCULAR MOLECULES FOR USE IN
; FILE REFERENCE: DEKM:176US
; CURRENT APPLICATION NUMBER: US/09/957,660
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 16
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-957-660-4
Query Match      100.0%; Score 13; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
Db      13 TATACGAACGGTA 1

RESULT 7
US-10-118-231-18
; Sequence 18, Application US/10118231
; Publication No. US20030005478A1
; GENERAL INFORMATION:
; APPLICANT: Bigger, Brian W
; APPLICANT: Tolmachov, Oleg
; APPLICANT: Coutelle, Charles
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 102286.141US
; CURRENT APPLICATION NUMBER: US/10/118,231
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/327,029
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: GB 0108968.9
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Construct
US-10-118-231-18
Query Match      100.0%; Score 13; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
Db      22 TATACGAACGGTA 34

RESULT 8
US-10-214-722-1
; Sequence 1, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; TITLE OF INVENTION: consecutive recombination-mediated recombinations
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 34
; TYPE: DNA
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide lox 66 without flanks
US-10-214-722-1
Query Match      100.0%; Score 13; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
Db      22 TATACGAACGGTA 34

RESULT 9
US-10-214-722-6/c
; Sequence 6, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; TITLE OF INVENTION: consecutive recombination-mediated recombinations
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide lox 71 without flanks
US-10-214-722-6
Query Match      100.0%; Score 13; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATACGAACGGTA 13
Db      13 TATACGAACGGTA 1

RESULT 10
US-10-214-722-8/c
; Sequence 8, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; TITLE OF INVENTION: consecutive recombination-mediated recombinations
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-214-722-8
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Query Match      100.0%; Score 13; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13
   |||||
Db 13 TATACGAACGGTA 1

RESULT 11
US-10-416-995-9
; Sequence 9, Application US/10416995
; Publication No. US20040077089A1
; GENERAL INFORMATION:
; APPLICANT: Xin, Hong-Bo
; APPLICANT: Kotlikoff, Michael
; TITLE OF INVENTION: CORNELL RESEARCH FOUNDATION, INC.
; FILE REFERENCE: 1153.020US1
; CURRENT APPLICATION NUMBER: US/10/416,995
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: PCT/US01/43916
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,200
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
; SEQ ID NO 9
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A mutant loxp sequence
US-10-416-995-9

Query Match      100.0%; Score 13; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13
   |||||
Db 22 TATACGAACGGTA 34

RESULT 12
US-10-416-995-10
; Sequence 10, Application US/10416995
; Publication No. US20040077089A1
; GENERAL INFORMATION:
; APPLICANT: Xin, Hong-Bo
; APPLICANT: Kotlikoff, Michael
; TITLE OF INVENTION: CORNELL RESEARCH FOUNDATION, INC.
; FILE REFERENCE: 1153.020US1
; CURRENT APPLICATION NUMBER: US/10/416,995
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: PCT/US01/43916
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,200
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
; SEQ ID NO 10
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A mutant loxp sequence
US-10-416-995-10

Query Match      100.0%; Score 13; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13
   |||||
Db 22 TATACGAACGGTA 34

RESULT 13
US-10-739-769-2
; Sequence 2, Application US/10739769
; Publication No. US20040137624A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; TITLE OF INVENTION: METHODS OF SITE-DIRECTED TRANSFORMATION
; FILE REFERENCE: 38-15(52823)B
; CURRENT APPLICATION NUMBER: US/10/739,769
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: variant of wild type loxp recombinase site
US-10-739-769-2

Query Match      100.0%; Score 13; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13
   |||||
Db 22 TATACGAACGGTA 34

RESULT 14
US-10-739-769-3/c
; Sequence 3, Application US/10739769
; Publication No. US20040137624A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; TITLE OF INVENTION: METHODS OF SITE-DIRECTED TRANSFORMATION
; FILE REFERENCE: 38-15(52823)B
; CURRENT APPLICATION NUMBER: US/10/739,769
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: variant of wild-type loxp recombination site
US-10-739-769-3

Query Match      100.0%; Score 13; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13
   |||||
Db 13 TATACGAACGGTA 1

RESULT 15
US-10-739-769-4
; Sequence 4, Application US/10739769
; Publication No. US20040137624A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; TITLE OF INVENTION: METHODS OF SITE-DIRECTED TRANSFORMATION
; FILE REFERENCE: 38-15(52823)B
```

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; CURRENT APPLICATION NUMBER: US/10/739,769
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: variant of wild-type loxP recombination site
US-10-739-769-4

Query Match      100.0%; Score 13; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TATACGAACGGTA 13
        |||||
Db      22 TATACGAACGGTA 34

Search completed: December 24, 2004, 11:42:15
Job time : 222.5 secs

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This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 08:02:10 ; Search time 1774.5 Seconds
(without alignments)
266.958 Million cell updates/sec

Title: US-10-030-658B-2

Perfect score: 13

Sequence: 1 tatacgaacgga 13

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821986908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_brc.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_ges1.*
- 9: gb_ges2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	100.0	233	8	BH855321 SALK_0859
2	13	100.0	288	2	AW927382 945017D12
3	13	100.0	308	2	AW927383 945017D12
C 4	13	100.0	313	9	AJ592954 Arabidops
5	13	100.0	367	5	BM964186 UI-M-EQ0
C 6	13	100.0	438	8	AQ711172 HS 5376 B
7	13	100.0	468	8	AQ650435 Sheared_D
C 8	13	100.0	490	8	AQ204576 HS 3229 B
9	13	100.0	498	2	AW682787 SWD25CAU
10	13	100.0	504	9	CL734978 OR_BBA006
C 11	13	100.0	505	6	CB408882 IFG018D06
12	13	100.0	534	4	BI455837 603171055
13	13	100.0	539	4	BM889392 OB_Ba005
C 14	13	100.0	553	9	CL598552 OB_Ba005
15	13	100.0	595	8	AQ574962 nbx0086B
16	13	100.0	606	5	BQ380889 KK32C07.Y
C 17	13	100.0	619	8	AQ649203 Sheared D
C 18	13	100.0	668	8	BH945623 obu75e01
C 19	13	100.0	669	8	AQ498235 HS 5104 A
C 20	13	100.0	708	9	CL599162 OB_Ba006
C 21	13	100.0	709	7	CF8117293 EST694675
22	13	100.0	761	5	BW455623 BM455623
C 23	13	100.0	806	9	AG098437 Pan trogl
24	13	100.0	896	9	AG508374 Mus muscu

25	13	100.0	900	4	BG400144
26	13	100.0	915	7	CF548337
C 27	13	100.0	924	6	CB561239
28	13	100.0	982	9	CNS06H7X
C 29	13	100.0	1020	9	CNS006D9
30	13	100.0	1118	9	AG511186
31	13	100.0	1286	5	BU326180
32	13	100.0	2306	9	CL511272
33	13	100.0	2945	7	CO760796
34	13	100.0	2945	7	CO760796
35	12	92.3	124	5	BM966340
C 36	12	92.3	131	9	CC882306
C 37	12	92.3	162	9	EX948525
38	12	92.3	167	8	CC104285
C 39	12	92.3	171	2	BB052078
C 40	12	92.3	185	8	BH896578
C 41	12	92.3	206	1	AV363052
C 42	12	92.3	229	8	AQ473103
43	12	92.3	237	2	BE525828
C 44	12	92.3	237	3	CNS08GBR
C 45	12	92.3	242	5	BW042380
	12	92.3	250	7	CN800693

ALIGNMENTS

RESULT 1
BH855321
LOCUS
DEFINITION
SALK_085977.20.05.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_085977.20.05.x, genomic
survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BH855321
BH855321.1
GI:21704911
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrianab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)

JOURNAL
COMMENT

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.

FEATURES
source

Class: TDNA tagged,
Location/Qualifiers
1..233
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_085977.20.05.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

Query Match 100.0%; Score 13; DB 8; Length 233;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13
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 Db 1.09 TATACGAACGGTA 121

RESULT 2
 AW927382
 LOCUS 945017D12.X1 945 - Mixed adult tissues from Walbot lab, same as 707
 DEFINITION (SK) Zea mays cDNA, mRNA sequence.
 ACCESSION AW927382
 VERSION AW927382.1 GI:8102741
 KEYWORDS EST.
 SOURCE Zea mays

ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 288)
 AUTHORS Walbot, V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 COMMENT University
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 945017 row: D column: 12.

FEATURES
 source
 1..288
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /tissue_type="tassel, kernal, silk, husk, root, leaf"
 /dev_stage="fully-grown"
 /lab_host="DH10B"
 /clone_lib="945 - Mixed adult tissues from Walbot lab,
 same as 707 (SK)"
 /note="Organ: tassel, kernal, silk, husk, root, leaf;
 Vector: pGAD10; Site 1: EcoRI; cDNA library from fully
 differentiated maize tissues from an active Mutator plant.
 Tissue ratio is 4:2:1:1:1 (tassel, kernal, silk, husk,
 root, leaf). Unidirectionally cloned. New library number
 given to library 707 for additional sequencing."

ORIGIN
 Query Match 100.0%; Score 13; DB 2; Length 288;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13
 |||||
 Db 46 TATACGAACGGTA 59

RESULT 3
 AW927383
 LOCUS 945017D12.X2 945 - Mixed adult tissues from Walbot lab, same as 707
 DEFINITION (SK) Zea mays cDNA, mRNA sequence.
 ACCESSION AW927383
 VERSION AW927383.1 GI:8102742
 KEYWORDS EST.
 SOURCE Zea mays

ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 288)
 AUTHORS Walbot, V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 COMMENT University
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 945017 row: D column: 12.

FEATURES
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 1..288
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /tissue_type="tassel, kernal, silk, husk, root, leaf"
 /dev_stage="fully-grown"
 /lab_host="DH10B"
 /clone_lib="945 - Mixed adult tissues from Walbot lab,
 same as 707 (SK)"
 /note="Organ: tassel, kernal, silk, husk, root, leaf;
 Vector: pGAD10; Site 1: EcoRI; cDNA library from fully
 differentiated maize tissues from an active Mutator plant.
 Tissue ratio is 4:2:1:1:1 (tassel, kernal, silk, husk,
 root, leaf). Unidirectionally cloned. New library number
 given to library 707 for additional sequencing."

ORIGIN
 Query Match 100.0%; Score 13; DB 2; Length 288;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13
 |||||
 Db 46 TATACGAACGGTA 59

RESULT 3
 AW927383
 LOCUS 945017D12.X2 945 - Mixed adult tissues from Walbot lab, same as 707
 DEFINITION (SK) Zea mays cDNA, mRNA sequence.
 ACCESSION AW927383
 VERSION AW927383.1 GI:8102742
 KEYWORDS EST.
 SOURCE Zea mays

ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 288)
 AUTHORS Walbot, V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 COMMENT University
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 945017 row: D column: 12.

FEATURES
 source
 1..288
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /tissue_type="tassel, kernal, silk, husk, root, leaf"
 /dev_stage="fully-grown"
 /lab_host="DH10B"
 /clone_lib="945 - Mixed adult tissues from Walbot lab,
 same as 707 (SK)"
 /note="Organ: tassel, kernal, silk, husk, root, leaf;
 Vector: pGAD10; Site 1: EcoRI; cDNA library from fully
 differentiated maize tissues from an active Mutator plant.
 Tissue ratio is 4:2:1:1:1 (tassel, kernal, silk, husk,
 root, leaf). Unidirectionally cloned. New library number
 given to library 707 for additional sequencing."

ORIGIN
 Query Match 100.0%; Score 13; DB 2; Length 288;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13
 |||||
 Db 46 TATACGAACGGTA 59

RESULT 3
 AW927383
 LOCUS 945017D12.X2 945 - Mixed adult tissues from Walbot lab, same as 707
 DEFINITION (SK) Zea mays cDNA, mRNA sequence.
 ACCESSION AW927383
 VERSION AW927383.1 GI:8102742
 KEYWORDS EST.
 SOURCE Zea mays

ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade; Panicoideae; Andropogoneae; Zea.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 308)
 AUTHORS Walbot, V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 COMMENT University
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 945017 row: D column: 12.

FEATURES
 Location/Qualifiers
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 /mol_type="mRNA"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /tissue_type="tassel, kernal, silk, husk, root, leaf"
 /dev_stage="fully-grown"
 /lab_host="DH10B"
 /clone_lib="945 - Mixed adult tissues from Walbot lab,
 same as 707 (SK)"
 /note="Organ: tassel, kernal, silk, husk, root, leaf;
 Vector: pGAD10; Site 1: EcoRI; cDNA library from fully
 differentiated maize tissues from an active Mutator plant.
 Tissue ratio is 4:2:1:1:1 (tassel, kernal, silk, husk,
 root, leaf). Unidirectionally cloned. New library number
 given to library 707 for additional sequencing."

ORIGIN
 Query Match 100.0%; Score 13; DB 2; Length 308;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13
 |||||
 Db 28 TATACGAACGGTA 40

RESULT 4
 AU592954/c
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 DEFINITION 372D03, genomic survey sequence.
 ACCESSION AJ592954
 VERSION AJ592954.1 GI:37942578
 KEYWORDS GSS; left border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1
 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
 Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
 Lepiniec, L., Caboche, M. and Lecharny, A.
 T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
 MEDLINE 22363535
 PUBMED 12446565
 REFERENCE 2 (bases 1 to 313)
 AUTHORS Balzergue, S.
 TITLE Direct Submission

JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
 Gaston Cremieux, 91057 Evry cedex, FRANCE
 COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment(s) resulting from

the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.verailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES

source
1. .313
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassiljewski1a"
/db_xref="taxon:3702"
/clone="372D03"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature
1. .313
/note="T-DNA flanking sequence
left border"

ORIGIN

Query Match 100.0%; Score 13; DB 9; Length 313;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13

Db 48 TATACGACGGTA 36

RESULT 5

BM964186 367 bp mRNA linear EST 18-MAR-2002
LOCUS UI-M-EQO-bvu-m-01-0-UI.r1 NIH_BMAP_EQO Mus musculus cDNA clone
DEFINITION IMAGE:5697192 5', mRNA sequence.

ACCESSION BM964186

VERSION BM964186.1 GI:19547606

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 367)

REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

Location/Qualifiers

FEATURES

source
1. .367
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5697192"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="NIH_BMAP_EQO"
/note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCAGCAG. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 100.0%; Score 13; DB 5; Length 367;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13

Db 262 TATACGACGGTA 274

RESULT 6

AQ7111712/c

LOCUS

DEFINITION HS 5376 B1_F05 SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=952 Col=9 Row=L, genomic survey sequence.

ACCESSION AQ7111712

VERSION AQ7111712.1 GI:5461028

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

MEDLINE 99380589

PUBMED 10449764

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/bac.htm>)or from Resear h Genetics (info@resgen.com). BAC end Web Server:<http://www.htsc.washington.edu>

Plate: 952 row: L column: 9

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 438.

FEATURES

source

Location/Qualifiers

1. .438

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=952 Col=9 Row=L"

/sex="male"

/clone_lib="RPCI-11 Human Male BAC Library"

/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;

Male blood DNA was isolated from one randomly chosen donor

and partially digested with a combination of EcoRI and

EcoRI Methylase. Size selected DNA was cloned into the

ORIGIN pBACE3.6 vector at EcoRI sites"

Query Match 100.0%; Score 13; DB 8; Length 438;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13
 |||||
 Db 135 TATACGAACGGTA 123

RESULT 7

AQ650435 468 bp DNA linear GSS 22-JUN-1999
 LOCUS Sheared DNA-18F1.TF Sheared DNA Trypanosoma brucei genomic clone
 DEFINITION Sheared DNA-18F1, genomic survey sequence.

ACCESSION AQ650435
 VERSION
 KEYWORDS
 SOURCE

ORGANISM

Trypanosoma brucei
 Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE

1 (bases 1 to 468)
 AUTHORS El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C.,
 Gerrard, C., Leach, V., de Jong, P., Ullu, E., Melville, S.,
 Donelson, J., Fraser, C. and Adams, M.

TITLE

Determination of clone end sequences from Trypanosoma brucei GUTat
 10.1 sheared DNA library

JOURNAL

Unpublished (1999)

COMMENT

Contact: Najib M. El-Sayed
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: nelsayed@tigr.org

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
 DNA library constructed at TIGR. Clones will be available for
 distribution through ATCC. Sheared DNA end sequences search page:
<http://www.tigr.org/tldb/mdb/tbdb/>.

Seq primer: M13-Forward

Class: Shotgun.

FEATURES

source

1..468
 Location/Qualifiers
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927/4 GUTat 10.1"
 /db_xref="taxon:5691"
 /clone="Sheared DNA-18F1"
 /clone_lib="Sheared DNA"
 /note="Vector: pUC18; Site 1: SmaI; Constructed at The
 Institute for Genomic Research (TIGR), Rockville, MD.
 Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
 sheared to give a tight size distribution (approx 2 kb).
 The v + i method used for the library construction is
 described in detail in Smith, H.O. and Venter, J.C.
 (Making small insert libraries for whole genome shotgun
 sequencing projects. In Genome Sequencing: A Practical
 Approach, eds. M. Vaudin and B. Borell, Oxford University
 Press, 1999)."

ORIGIN.

Query Match 100.0%; Score 13; DB 8; Length 468;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13
 |||||
 Db 84 TATACGAACGGTA 96

RESULT 8

AQ204576/c

LOCUS

DEFINITION

HS_3229_B1_B09_T7 CIT Approved Human Genomic Sperm Library D Homo

sapiens genomic clone Plate=3229 Col=17 Row=D, genomic survey

sequence.

ACCESSION AQ204576

VERSION AQ204576

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 490)

AUTHORS

Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,

Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and

Hood, L.

TITLE

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

MEDLINE

99380599

PUBMED

10449764

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Sequence Tagged Connector

Plate: 3229 Row: D Column: 17

Class: BAC ends

High quality sequence stop: 490.

Location/Qualifiers

1..490

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=3229 Col=17 Row=D"

/sex="male"

/clone_lib="CIT Approved Human Genomic Sperm Library D"

/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in

E-Coli DH10B"

ORIGIN

Query Match 100.0%; Score 13; DB 8; Length 490;

Best Local Similarity 100.0%; Pred. No. 5.8e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13

|||||

Db 29 TATACGAACGGTA 17

|||||

RESULT 9

AW682787

LOCUS

DEFINITION

SWYD25CAUI3A03SK Brugia malayi young adult day 25 cDNA

(SAW99MLW-BmYD25) Brugia malayi cDNA clone SWYD25CAUI3A03 5', mRNA

sequence.

ACCESSION AW682787

VERSION AW682787.1 GI:7557489

KEYWORDS

EST.

SOURCE

Brugia malayi

Brugia malayi

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;

Onchocercidae; Brugia.

1 (bases 1 to 498)

REFERENCE

1 (bases 1 to 498)

AUTHORS

Williams, S.A.

TITLE

Genes expressed in young adult day 25 of Brugia malayi

Unpublished (1999)

JOURNAL

COMMENT
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
source
1..498
/organism="Brugia malayi"
/mol_type="mRNA"
/db_xref="taxon:6279"
/clone="SWYD25CAU13A03"
/dev_stage="young adult, twenty five days after infection"
/lab_host="XLI-Blue MRP,"
/clone_lib="Brugia malayi young adult day 25 cDNA
(SAW99MLW-BmyD25)"
/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:
Xho I; Lymphatic filarial nematode parasite of humans.
mRNA was prepared from young adult worms isolated from
the peritoneal cavity of birds on day 25 after infection
and converted to double-stranded cDNA using reverse
transcriptase and oligo(dT) followed by RNase H and DNA
pol I. The library has 6.2 x 105 independent recombinants
and the average insert size is approx.1101bp. The library
was constructed by Michelle Lizotte-Waniewski. The
library is available from Dr. S.A. Williams, email:
genome@neal.smith.edu."

ORIGIN
Query Match 100.0%; Score 13; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13
|||||
Db 172 TATACGAACGGTA 184
|||||

RESULT 10
CL734978 504 bp DNA linear GSS 27-JUL-2004
LOCUS OR_BBa0068F22.r OR_BBa Oryza rufipogon genomic clone OR_BBa0068F22
DEFINITION 3'- genomic survey' sequence.
ACCESSION CL734978
VERSION CL734978.1 GI:50669334
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartodeae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 504)
AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0068 row: F column: 22
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source
1..504
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_BBa0068F22"
/tissue type="young leaves"
/lab host="DH10B-T1 phage resistant"
/clone_lib="OR_BBa"
/note="Vector: PAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match 100.0%; Score 13; DB 9; Length 504;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13
|||||
Db 56 TATACGAACGGTA 68
|||||

RESULT 11
CB408882/c 505 bp mRNA linear EST 24-OCT-2003
LOCUS IPG018D06 250666 JH III-treated male I. pini midguts Ips pini cDNA
DEFINITION clone IPG018D06 5, mRNA sequence.
ACCESSION CB408882
VERSION CB408882.1 GI:37953018
KEYWORDS EST.
SOURCE Ips pini (North American pine engraver)
ORGANISM Ips pini
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Scolytidae; Ips.
REFERENCE 1 (bases 1 to 505)
AUTHORS Eigenheer,A.L., Keeling,C.I., Young,S. and Tittiger,C.
TITLE Comparison of gene representation in midguts from two phytophagous
insects, Bombyx mori and Ips pini, using expressed sequence tags
JOURNAL Gene 316, 127-136 (2003)
MEDLINE 22925480
PubMed 14563559
COMMENT Contact: Tittiger C
Biochemistry Department
University of Nevada, Reno
Howard Medical Sciences Rm. 150, Reno, NV 89557, USA
Tel: 1-775-784-6480
Fax: 1-775-784-1419
Email: crt@unr.edu
PCR Primers
FORWARD: T3 21mer
BACKWARD: T7 21mer (backward)
Plate: 018 row: D column: 06
Seq primer: T3 21mer
High quality sequence stop: 505.
Location/Qualifiers
source
1..505
/organism="Ips pini"
/mol_type="mRNA"
/db_xref="taxon:102803"
/clone="IPG018D06"
/sex="male"
/tissue type="midgut"
/dev stage="adult"
/clone_lib="JH III-treated male I. pini midguts"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; As per
Stratagene's pBluescript II XR library construction kit"

FEATURES
source
1..505
/organism="Ips pini"
/mol_type="mRNA"
/db_xref="taxon:102803"
/clone="IPG018D06"
/sex="male"
/tissue type="midgut"
/dev stage="adult"
/clone_lib="JH III-treated male I. pini midguts"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; As per
Stratagene's pBluescript II XR library construction kit"

ORIGIN
Query Match 100.0%; Score 13; DB 6; Length 505;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13

```

Db      78 TATACGAACGGTA 66

RESULT 12
LOCUS   BI455837
DEFINITION 603171055F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5250637 5',
mRNA sequence.
ACCESSION BI455837
VERSION   BI455837.1 GI:15246493
KEYWORDS  Mus musculus (house mouse)
SOURCE   Mus musculus
ORGANISM Mus musculus
REFERENCE
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 534)
TITLE     NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L14M1632 row: n column: 14
High quality sequence stop: 534.
Location/Qualifiers
1..534
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5250637"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Mam5"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

ORIGIN
Query Match 100.0%; Score 13; DB 4; Length 534;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13
|||||
Db 474 TATACGAACGGTA 486

RESULT 13
LOCUS   BM889392
DEFINITION Xb09h04.y1 Brugia malayi 2D L3 irradiated pAMP1 v1 Brugia malayi
cDNA 5', similar to WP:CE25594 Y73F8A.26 i, mRNA sequence.
ACCESSION BM889392
VERSION   BM889392.1 GI:19298139
KEYWORDS  Brugia malayi
SOURCE   Brugia malayi
ORGANISM Brugia malayi
REFERENCE
AUTHORS   Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
1 (bases 1 to 539)
TITLE     McCarter, J., Clifton, S., Chiappelli, B., Pape, D., Martin, J.,
Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, B., Bennett, J., Franklin, C.,
Tsagaris, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Amy Hofer, Claire Murphy and Dr.
James McCarter at Washington University, St. Louis. DNA Sequencing
by: Washington University Genome Sequencing Center
High quality sequence stop: 395.
Location/Qualifiers
1..539
/organism="Brugia malayi"
/mol_type="mRNA"
/db_xref="taxon:6279"
/dev_stage="irradiated 2 day cultured L3"
/lab_host="DH10B"
/clone_lib="Brugia malayi 2D L3 irradiated pAMP1 v1"
/notes="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
The library was constructed by Amy Hofer, Claire Murphy
and Dr. James McCarter at Washington University, St.
Louis. The cDNA was made by using Dynabead oligo-dT
priming (Dynal). PCR based library using a modified
protocol from the SMART PCR cDNA Synthesis Kit from
Clontech. Directionally cloned into the UDG sites of
pAMP1. Irradiated and cultured nematodes were provided by
Dr. Ben-Wen Li and Dr. Gary Weil of Washington University,
St. Louis, MO (weillab@imgate.wustl.edu)."

ORIGIN
Query Match 100.0%; Score 13; DB 4; Length 539;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGAACGGTA 13
|||||
Db 192 TATACGAACGGTA 204

RESULT 14
LOCUS   CL598552/c
DEFINITION OB_BA0060009.f OB_Ba Oryza brachyantha genomic clone
OB_BA0060009 5', genomic survey sequence.
ACCESSION CL598552
VERSION   CL598552.1 GI:48572791
KEYWORDS  GSS.
SOURCE   Oryza brachyantha
ORGANISM Oryza brachyantha
REFERENCE
AUTHORS   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 553)
TITLE     Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers

```

FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Insert Length: 145000 Std Error: 0.00
 Plate: 0060 row: 0 column: 09
 Seq primer: TAA TAC GAC TCA CTA TAG GG
 Class: BAC ends.

FEATURES

source

Location/Qualifiers
 1. 553
 /organism="Oryza brachyantha"
 /mol_type="genomic DNA"
 /db_xref="taxon:4533"
 /clone="OB_Ba0060009"
 /tissue_type="leaves"
 /dev_stage="mature"
 /lab_host="DH10B"
 /clone_lib="OB_Ba"
 /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 100.0%; Score 13; DB 9; Length 553;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13

|||||

Db 529 TATACGAACGGTA 517

RESULT 15

AQ574962

LOCUS

DEFINITION

AQ574962 595 bp DNA linear GSS 02-JUN-1999
 nbxb0086B17f CUGI Rice BAC Library Oryza sativa (japonica
 cultivar-group) genomic clone nbxb0086B17f, genomic survey
 sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 595)
 Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Rice Genome
 Unpublished (1998)
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu

Seq primer: TAATACGACTCACTATAGGG

Class: BAC ends

High quality sequence stop: 201.

FEATURES

source

Location/Qualifiers
 1. 595
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="genomic DNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="nbxb0086B17f"
 /tissue_type="Leaf"
 /lab_host="E. coli DH10B"
 /clone_lib="CUGI Rice BAC Library"

/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
 HindIII; Rice is one of two most popular grains in the
 world. Half of the world population especially those
 inhabiting highly populated areas of the humid tropics
 and subtropics, rely on rice as their primary source of
 carbohydrate. Monocotyledonous rice is a diploid plant
 (2n=24) with a haploid genome equivalent of 431 Mbp

(Arumuganathan and Earle, 1991). The relatively small
 genome of rice, three times larger than that of
 Arabidopsis, makes it suitable for genomic studies. In
 order to facilitate positional cloning, physical mapping
 and genome sequencing of rice, we have constructed a BAC
 library from Oryza sativa, Nipponbare variety. The
 library contains 36,864 clones with an average insert size
 of 128.5 Kb providing 10.9 haploid genome equivalents. The
 deep coverage allows the isolation a particular sequence
 with a probability of 99.9 %. Two high density filters,
 each containing 18,432 clones (doubly spotted), represent
 the whole library for colony screening."

ORIGIN

Query Match 100.0%; Score 13; DB 8; Length 595;

Best Local Similarity 100.0%; Pred. No. 5.9e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATACGAACGGTA 13

|||||

Db 56 TATACGAACGGTA 68

Search completed: December 24, 2004, 10:11:14

Job time : 1774.5 secs

619-594-3336 Mike Rondelli.